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OM protein - protein search, using sw model

Run on: September 20, 2002, 10:27:17 ; Search time 30 Seconds
(without alignments)
66.644 Million cell updates/sec

Title: US-08-854-764-7

Perfect score: 96
Sequence: 1 DSEDEHTITDTLPP 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_032802:*

- 1: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT:*
- 2: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT:*
- 3: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT:*
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- 6: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT:*
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- 8: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT:*
- 9: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT:*
- 10: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT:*
- 11: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT:*
- 12: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT:*
- 13: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT:*
- 14: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT:*
- 15: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT:*
- 16: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT:*
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- 19: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT:*
- 20: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT:*
- 21: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT:*
- 22: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	96	100.0	18	AA92013	TFPI N-terminal pe
2	96	100.0	160	AA23800	LACI fragment 1 -
3	96	100.0	161	AAW00017	TFPI chimeric prot
4	96	100.0	225	AAU02971	Angiotensin conver
5	96	100.0	256	AA111169	Ser(Asp1-Thr255)-E
6	96	100.0	261	AA111171	Ser-(Asp1-Glu245)-
7	96	100.0	262	AA111172	Ser-(Asp1-Ser248)-
8	96	100.0	265	AA111170	Ser-(Asp1-Ile253)-
9	96	100.0	276	AA922265	TFPI mutin, Lys36
10	96	100.0	276	AA92012	TFPI mutin K36R.
11	96	100.0	276	AAW30311	Recombinant non-g1

12	96	100.0	276	19	AAW61535	Human tissue facto
13	96	100.0	277	14	AA37312	Non-glycosylated T
14	96	100.0	304	10	AA92002	Human tissue facto
15	96	100.0	304	16	AA81884	Lipoprotein-associ
16	96	100.0	304	16	AA878389	Human lipoprotein-
17	96	100.0	304	16	AA867994	Tissue factor path
18	96	100.0	304	20	AA49557	Human lipoprotein
19	96	100.0	352	17	AA92011	Ubiquitin-TFPI fus
20	93	96.9	304	21	AA70272	Human mutant tissu
21	93	96.9	304	21	AA70273	Human tissue facto
22	90	93.8	189	12	AA111167	(Asp1-Thr161)-EPI
23	90	93.8	304	14	AA42309	LACI gene product.
24	86	89.6	23	15	AA55840	LACI N-terminal (G
25	50.5	52.6	224	18	AA36796	Novel human protei
26	49	51.0	1036	22	AA85011	Shrimp white spot
27	48	50.0	22	14	AA37859	Tissue factor inh1
28	48	50.0	22	15	AA63232	Tissue factor inac
29	48	50.0	22	16	AA95880	Tissue factor inh1
30	47	49.0	1085	17	AA95607	RRP3 telomerase-as
31	47	49.0	1189	18	AA26623	Signalling inosito
32	46	47.9	111	21	AA45731	Arabidopsis thalia
33	46	47.9	118	21	AA17608	Arabidopsis thalia
34	46	47.9	125	21	AA45730	Arabidopsis thalia
35	46	47.9	198	21	AA95939	Porcine adenovirus
36	46	47.9	467	21	AA45700	Arabidopsis thalia
37	46	47.9	759	22	AAU15066	Protein encoded by
38	46	47.9	831	22	ABG01620	Novel human diagno
39	46	47.9	831	22	ABG03191	Novel human diagno
40	46	47.9	1492	22	ABG14001	Novel human diagno
41	46	47.9	2670	17	AA88125	Rat IP3 receptor.
42	45	46.9	406	20	AA34969	Chlamydia pneumoni
43	45	46.9	423	22	AA25908	Human protein sequ
44	45	46.9	570	18	AA36002	Human Fchd531 gene
45	45	46.9	570	21	AA45013	Protein encoded by

ALIGNMENTS

RESULT 1

AA92013

ID AAR92013 standard; Peptide: 18 AA.

XX

AC AAR92013;

XX

DT 08-MAY-1996 (first entry)

XX

DE TFPI N-terminal peptide.

XX

KW Tissue factor pathway inhibitor; TFPI; TFPI-2; Factor-VIIa;

KW tissue factor; Factor-Xa; binding protein; tissue factor inhibitor;

KW lipoprotein associated coagulation inhibitor;

KW extrinsic pathway inhibitor; sepsis; septic shock;

KW Saccharomyces cerevisiae.

OS Synthetic.

XX

PN WO9604377-AL.

XX

PD 15-FEB-1996.

XX

PF 25-JUL-1995; 95WO-US09377.

XX

PR 05-AUG-1994; 94US-0286530.

XX

PA (CHIR) CHIRON CORP.

XX

PI Creasey AA, Innis MA;

XX

DR WPI; 1996-129393/13.

XX

PT Production of tissue factor pathway inhibitor in yeast cells - with isolation from the insoluble cell fraction, used to treat or prevent

PT sepsis or septic shock
 XX
 PS Example 2; Page 16; 36pp; English.
 XX
 CC The N-terminal peptide (AAR92013) of recombinant tissue factor
 CC pathway inhibitor (TFPI) produced in *Saccharomyces cerevisiae*
 CC cells transformed with vector plasmid pLACI 4.1 corresponded
 CC to authentic mature TFPI. This showed that expression of a
 CC ubiquitin/TFPI protein fusion in yeast, with subsequent
 CC removal of the ubiquitin fusion partner within the yeast cells,
 CC provided biologically active TFPI having the correct N-terminal
 CC sequence.
 XX
 SQ Sequence 18 AA;
 Query Match 100.0%; Score 96; DB 17; Length 18;
 Best Local Similarity 100.0%; Pred. No. 4e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 DSEEDERTITDTELP 18
 ||||||||||||||||
 Db 1 dseedehtitdtelp 18
 RESULT 2
 ID AAR23800; AAR23800 standard; Protein: 160 AA.
 AC AAR23800;
 XX
 DT 03-NOV-1992 (first entry)
 XX
 DE LACI fragment 1 - 160.
 XX
 KW Lipoprotein-associated coagulation inhibitor: kunitz.
 XX
 OS Homo sapiens.
 OS
 XX
 PN USS106833-A.
 XX
 PD 21-APR-1992.
 XX
 PF 26-JAN-1989; 89US-0301779.
 XX
 PR 23-JUL-1987; 87US-0077366.
 PR 23-NOV-1987; 87US-0123753.
 PR 26-JAN-1989; 89US-0301779.
 XX
 PA (UNIT) UNIV WASHINGTON.
 PI Broze GJ, Girard TJ;
 PI
 DR WPI; 1992-159405/19.
 XX
 PT Peptide fragments of lipoprotein-associated coagulation inhibitor
 PT - used for inhibiting Factor Xa prodn. or inhibiting Factor VIIA
 PT tissue factor complex formation
 PT
 XX
 PS Disclosure; Fig 1; 9pp; English.
 XX
 CC The sequence given is a peptide fragment of lipoprotein-associated
 CC coagulation inhibitor (LACI) having the sequence of residues 1
 CC to 160 of the 276 residue mature LACI protein. This peptide fragment
 CC corresponds to kunitz domains of LACI and can be used for
 CC inhibiting Factor VIIA/tissue factor enzymatic complex formation.
 CC
 CC Factor VIIA is the activated form of Factor VII.
 CC
 XX
 SQ Sequence 160 AA;
 Query Match 100.0%; Score 96; DB 13; Length 160;
 Best Local Similarity 100.0%; Pred. No. 4.5e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 DSEEDERTITDTELP 18
 ||||||||||||||||
 Db 1 dseedehtitdtelp 18
 RESULT 3
 ID AAM00017; AAM00017 standard; Protein: 161 AA.
 AC AAM00017;
 XX
 DT 30-SEP-1996 (first entry)
 XX
 DE TFPI chimeric protein.
 XX
 KW Kunitz-type domain; C-terminal tail; tissue factor pathway inhibitor;
 KW TFPI-2; cell surface localisation; glycosaminoglycan; heparin;
 KW phospholipid; binding; chimeric protein; mutein; substitution;
 KW PI-reactive site; sepsis; septic shock; thrombosis; up-regulation;
 KW tissue factor; injury; trauma; endotoxin; TNF; cancer; IL-1;
 KW tumour necrosis factor; interleukin.
 XX
 OS Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT Domain 26..76
 FT /note= "First Kunitz-type domain"
 FT Misc-difference 36
 FT /label= Lys36Arg
 FT Domain 97..147
 FT /note= "Second Kunitz-type domain"
 FT Misc-difference 117
 FT /label= Asn117Gln
 XX
 PN M09604378-A2.
 XX
 PD 15-FEB-1996.
 XX
 PF 25-JUL-1995; 95MO-US09464.
 XX
 PR 05-AUG-1994; 94US-0286521.
 XX
 PA (CHIR) CHIRON CORP.
 PI Creasey AA, Innis MA;
 PI
 DR WPI; 1996-129394/13.
 XX
 PT Chimeric protein comprising Kunitz-type domains from TFPI-1 and -2
 PT - used for the treatment of septic shock and thrombosis disorders
 PT
 XX
 PS Claim 14; Page 19; 68pp; English.
 XX
 CC This sequence represents a chimeric protein containing the first and
 CC second kunitz-type domain derived from tissue factor pathway inhibitor
 CC (TFPI). This sequence has a Lys to Arg mutation in the PI-reactive
 CC domain of the first Kunitz-type domain, and an Asn to Gln mutation in
 CC the PI-reactive domain of the second Kunitz-domain. The Kunitz-type
 CC domains are highly basic sequences and may be involved in cell surface
 CC localisation by glycosaminoglycan (including heparin) or phospholipid
 CC binding. Chimeric proteins such as this, having one or more
 CC substitutions exclusively in the PI-reactive site of one or more
 CC Kunitz-type domains are covered within the scope of the invention.
 CC Chimeric proteins comprising the kunitz-type domains from TFPI-1 or
 CC TFPI-2, may also comprise an alternative glycosaminoglycan binding
 CC peptide selected from those given in AAR92266-73. The chimeric proteins
 CC and muteins may be used in a pharmaceutical composition for the
 CC treatment of sepsis, septic shock and thrombosis disorders. The proteins
 CC may be generally useful in the treatment of diseases caused by the
 CC up-regulation of tissue factor brought on by injury, trauma, endotoxin,
 CC TNF, cancer, IL-1 or other agents or conditions.

XX
SQ Sequence 161 AA;

Query Match 100.0%; Score 96; DB 17; Length 161;
Best Local Similarity 100.0%; Pred. No. 4.6e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSEDEEHTITDTLPP 18
Db 1 dseedehtitdtelpp 18

RESULT 4

ID AAU02971 standard; Protein; 225 AA.

AC AAU02971;

DT 12-SEP-2001 (first entry)

DE Angiotensin converting enzyme (ACEV) splice variant protein #71.

XX
KW Angiotensin converting enzyme splice variant; ACEV; interleukin 6;
granulocyte colony stimulating factor receptor; glucagon; hypertrophy;
platelet-derived endothelial cell growth factor; cardiovascular disease;
cellular tumour antigen p53; cyclin-dependent kinase inhibitor 1C;
vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer;
myocardial infarction; coronary arterial thrombosis; renal disease;
diabetic nephropathy; muscular disease; immune disorder; sarcoidosis;
multiple sclerosis; immune complex nephritis; deep vein thrombosis;
nonarctoidotic pulmonary granulomatous disease; endothelial abnormality;
vascular disorder; asbestosis.

OS Homo sapiens.

XX WO200136632-A2.

PN 25-MAY-2001.

PD 17-NOV-2000; 2000WO-IL00766.

PF 17-NOV-1999; 99IL-0132978.

PR 10-DEC-1999; 99IL-0133455.

XX (COMP-) COMPUGEN LTD.

PA Levine Z, David A, Azar I, Khosravi R, Bernstein J;

PI WPI: 2001-336004/35.

DR N-PSDB; AAS06071.

XX Novel alternative splicing variants e.g. variant of angiotensin
converting enzyme (ACEV), useful in identifying candidate compounds
capable of binding to the variant and to detect anti-variant antibodies

PS Claim 4; Fig 71; 519pp; English.

XX The sequence represents an angiotensin converting enzyme splice variant
(ACEV) polypeptide. The polypeptides of the invention include variants of
granulocyte colony stimulating factor receptor, glucagon, interleukin 6,
platelet-derived endothelial cell growth factor, cyclin-dependent kinase
inhibitor 1C, cellular tumour antigen p53, and vasoactive intestinal
polypeptide receptor 2. The polypeptides and their associated nucleic
acids are useful for identification of variant sequences and detection of
candidate compounds capable of binding the molecules. The sequences of
the invention can be used in the treatment and diagnosis of various
disorders including cardiovascular diseases such as arteriosclerosis,
myocardial infarction and coronary arterial thrombosis, renal diseases
such as diabetic nephropathy, muscular diseases such as hypertrophy,
immune disorders such as immune complex nephritis, multiple sclerosis,
cancer, sarcoidosis, nonarctoidotic pulmonary granulomatous diseases such

CC as asbestosis and vascular pathologies involving an endothelial
CC abnormality such as deep vein thrombosis.
XX
SQ Sequence 225 AA;

Query Match 100.0%; Score 96; DB 22; Length 225;
Best Local Similarity 100.0%; Pred. No. 6.6e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSEDEEHTITDTLPP 18
Db 29 dseedehtitdtelpp 46

RESULT 5

ID AAR11169 standard; Protein; 256 AA.

AC AAR11169;

DT 21-MAY-1991 (first entry)

DE Ser(Asp1-Thr255)-EPI analogue.

XX
KW Extrinsic pathway inhibitor protein; tissue plasminogen activator;
kunitz domain; coagulation.

OS Synthetic.

XX WO9102753A1.

PN 07-MAR-1991.

PD 17-AUG-1990; 90WO-DK00212.

PF 18-AUG-1989; 89DK-0004080.

PR (NOVO) NOVO NORDISK A/S.

XX Rasmussen J, Nordfang O;

PI WPI: 1991-087248/12.

XX Extrinsic pathway inhibitor protein analogue - useful as
anticoagulant and anti-cancer agent due to low or no
heparin-binding capacity

PS Claim 5; Page 20; 39pp; English.

XX Preferred EPI analogues of the invention comprise the first two
kunitz domains of native EPI and have one or more amino acids
deleted in the region Glu148 to the C-terminal Met276, especially
in the region from Arg246 to Lys275. This analogue is an example of
such a peptide; it corresponds to amino acids 1 to 255 of native EPI
with an additional N-terminal Ser residue. The analogue can be used
in a therapeutic composition to treat patients having coagulation
disorders or cancer. The analogue has a longer half-life than
full-length EPI.
XX See also AAO10992-4 and AAR11170-R11172.

XX Sequence 256 AA;

Query Match 100.0%; Score 96; DB 12; Length 256;
Best Local Similarity 100.0%; Pred. No. 7.6e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSEDEEHTITDTLPP 18
Db 2 dseedehtitdtelpp 19

RESULT 6

AA11171
ID AA11171 standard; Protein: 261 AA.

XX
AC AA11171;

XX
DT 21-MAY-1991 (first entry)

XX
DE Ser-(Asp1-Glu245)-(Glu262-Met276)-EPI analogue.

XX
KM Extrinsic pathway inhibitor protein; tissue plasminogen activator;
XX kunitz domain; coagulation.

XX
OS Synthetic.

XX
PN WO9102753-A.

XX
PD 07-MAR-1991.

XX
PE 17-AUG-1990; 90WO-DK00212.

XX
PR 18-AUG-1989; 89DK-0004080.

XX
PA (NOVO) NOVO NORDISK A/S.

XX
PI Rasmussen J, Nordfang O;

XX
DR WPI; 1991-087248/12.

XX
PT Extrinsic pathway inhibitor protein analogue - useful as
PT anticoagulant and anti-cancer agent due to low or no
PT heparin-binding capacity

XX
PS Claim 5; Page 20; 39pp; English.

XX
CC Preferred EPI analogues of the invention comprise the first two
CC kunitz domains of native EPI and have one or more amino acids
CC deleted in the region Glu148 to the C-terminal Met276, especially
CC in the region from Arg246 to Lys275. This analogue is an example of
CC such a peptide; it has amino acids 246 to 261 of native EPI deleted
CC with an optional N-terminal Ser residue. The analogue can be used
CC in a therapeutic composition to treat patients having coagulation
CC disorders or cancer. The analogue has a longer half-life than
CC full-length EPI.

CC
CC See also AAQ10992-4 and AA11169-R11170,AA11172.

XX
SQ Sequence 261 AA;

Query Match

Best Local Similarity 100.0%; Score 96; DB 12; Length 261;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DSEDEEHTITITDTELP 18
Db 2 dseedehtittdelepp 19

RESULT 7

AA11172
ID AA11172 standard; Protein: 262 AA.

XX
AC AA11172;

XX
DT 21-MAY-1991 (first entry)

XX
DE Ser-(Asp1-Ser248)-(Val264-Met276)-EPI analogue.

XX
KM Extrinsic pathway inhibitor protein; tissue plasminogen activator;
XX kunitz domain; coagulation.

XX
OS Synthetic.

XX
PT Extrinsic pathway inhibitor protein analogue - useful as

PN WO9102753-A.

XX
PD 07-MAR-1991.

XX
PE 17-AUG-1990; 90WO-DK00212.

XX
PR 18-AUG-1989; 89DK-0004080.

XX
PA (NOVO) NOVO NORDISK A/S.

XX
PI Rasmussen J, Nordfang O;

XX
DR WPI; 1991-087248/12.

XX
PT Extrinsic pathway inhibitor protein analogue - useful as
PT anticoagulant and anti-cancer agent due to low or no
PT heparin-binding capacity

XX
PS Claim 5; Page 20; 39pp; English.

XX
CC Preferred EPI analogues of the invention comprise the first two
CC kunitz domains of native EPI and have one or more amino acids
CC deleted in the region Glu148 to the C-terminal Met276, especially
CC in the region from Arg246 to Lys275. This analogue is an example of
CC such a peptide; it has amino acids 249 to 263 of native EPI deleted
CC with an optional N-terminal Ser residue. The analogue can be used
CC in a therapeutic composition to treat patients having coagulation
CC disorders or cancer. The analogue has a longer half-life than
CC full-length EPI.

XX
CC See also AAQ10992-4 and AA11169-R11171.

XX
SQ Sequence 262 AA;

Query Match

Best Local Similarity 100.0%; Score 96; DB 12; Length 262;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DSEDEEHTITITDTELP 18
Db 2 dseedehtittdelepp 19

RESULT 8

AA11170
ID AA11170 standard; Protein: 265 AA.

XX
AC AA11170;

XX
DT 21-MAY-1991 (first entry)

XX
DE Ser-(Asp1-Ile253)-(Ile266-Met276)-EPI analogue.

XX
KM Extrinsic pathway inhibitor protein; tissue plasminogen activator;
XX kunitz domain; coagulation.

XX
OS Synthetic.

XX
PN WO9102753-A.

XX
PD 07-MAR-1991.

XX
PE 17-AUG-1990; 90WO-DK00212.

XX
PR 18-AUG-1989; 89DK-0004080.

XX
PA (NOVO) NOVO NORDISK A/S.

XX
PI Rasmussen J, Nordfang O;

XX
DR WPI; 1991-087248/12.

XX
PT Extrinsic pathway inhibitor protein analogue - useful as

PT anticoagulant and anti-cancer agent due to low or no
 PT heparin-binding capacity

PS Claim 5; Page 20; 39pp; English.

XX Preferred EPI analogues of the invention comprise the first two
 CC kunitz domains of native EPI and have one or more amino acids
 CC deleted in the region Glu148 to the C-terminal Met276, especially
 CC in the region from Arg246 to Lys275. This analogue is an example of
 CC such a peptide; it has amino acids 254 to 265 of native EPI deleted
 CC with an optional N-terminal Ser residue. The analogue can be used
 CC in a therapeutic composition to treat patients having coagulation
 CC disorders or cancer. The analogue has a longer half-life than
 CC full-length EPI.
 CC See also AAQ10992-4 and AAR11169, AAR11171-R11172.

XX Sequence 265 AA;

Query Match 100.0%; Score 96; DB 12; Length 265;
 Best Local Similarity 100.0%; Pred. No. 7.9e-07; Mismatches 0; Indels 0; Gaps 0;
 Matches 18; Conservative 0;

Qy 1 DSEDEDEHTIITDTELP 18
 Dp 2 DSEDEDEHTIITDTELP 19

RESULT 9

AAR92265
 ID AAR92265 standard; peptide; 276 AA.

AC AAR92265;

DT 30-SEP-1996 (first entry)

DE TFPI mutein, Lys36Arg.

KW Kunitz-type domain; C-terminal tail; tissue factor pathway inhibitor;
 KW TFPI; TFPI-2; cell surface localisation; glycosaminoglycan; heparin;
 KW phospholipid; binding; chimeric protein; mutein; substitution;
 KW PI-reactive site; sepsis; septic shock; thrombosis; up-regulation;
 KW tissue factor; injury; trauma; endotoxin; TNF; cancer; IL-1;
 KW tumour necrosis factor; interleukin.

OS Homo sapiens.

XX Key Location/Qualifiers
 XX Domain 26..76

FT Misc-difference 36 /note= "First Kunitz-type domain"

FT Domain /label= Lys36Arg

FT Domain 97..147

FT Domain /note= "Second Kunitz-type domain"

FT Domain 189..239

FT Domain /note= "Third Kunitz-type domain"

FT Domain 240..276

FT Domain /note= "C-terminal tail"

XX WO9604378-A2.

XX 15-FEB-1996.

XX 25-JUL-1995; 95WO-US09464.

XX 05-AUG-1994; 94US-0286521.

XX (CHIR) CHIRON CORP.

XX Creasey AA, Innis MA;

XX WPI; 1996-129394/13.

PT Chimeric protein comprising Kunitz-type domains from TPPI-1 and -2
 PT - used for the treatment of septic shock and thrombosis disorders

PS Disclosure; Page 8; 68pp; English.

XX This sequence represents a mutein of tissue factor pathway inhibitor
 CC (TFPI). This sequence has a Lys to Arg mutation in the PI-reactive
 CC domain of the first Kunitz-type domain. The Kunitz-type domains are
 CC highly basic sequences and may be involved in cell surface localisation
 CC by glycosaminoglycan (including heparin) or phospholipid binding.
 CC Muteins such as this, having one or more substitutions exclusively in
 CC the PI-reactive site of one or more Kunitz-type domains are covered by
 CC the scope of the invention. Chimeric proteins comprising the Kunitz-
 CC type domains from TPPI or TPPI-2, may also comprise an alternative
 CC glycosaminoglycan binding peptide selected from those given in
 CC AAR92266-73. The chimeric proteins and muteins may be used in a
 CC pharmaceutical composition for the treatment of sepsis, septic shock
 CC and thrombosis disorders. The proteins may be generally useful in the
 CC treatment of diseases caused by the up-regulation of tissue factor
 CC bought on by injury, trauma, endotoxin, TNF, cancer, IL-1 or other
 CC agents or conditions.

XX Sequence 276 AA;

Query Match 100.0%; Score 96; DB 17; Length 276;
 Best Local Similarity 100.0%; Pred. No. 8.3e-07; Mismatches 0; Indels 0; Gaps 0;
 Matches 18; Conservative 0;

Qy 1 DSEDEDEHTIITDTELP 18
 Dp 1 DSEDEDEHTIITDTELP 18

RESULT 10

AAR92012
 ID AAR92012 standard; Protein; 276 AA.

XX AAR92012;

DT 08-MAY-1996 (first entry)

DE TFPI mutein K36R.

KW Tissue factor pathway inhibitor; TPPI; TPPI-2; Factor-VIIa;
 KW tissue factor; Factor-Xa; binding protein; tissue factor inhibitor;
 KW lipoprotein associated coagulation inhibitor;
 KW extrinsic pathway inhibitor; sepsis; septic shock;
 KW Saccharomyces cerevisiae.

XX Synthetic.

XX WO9604377-A1.

XX 15-FEB-1996.

XX 25-JUL-1995; 95WO-US09377.

XX 05-AUG-1994; 94US-0286530.

XX (CHIR) CHIRON CORP.

XX Creasey AA, Innis MA;

XX WPI; 1996-129393/13.

XX Production of tissue factor pathway inhibitor in yeast cells - with
 XX isolation from the insoluble cell fraction, used to treat or prevent
 XX sepsis or septic shock

XX Disclosure; Page 9; 36pp; English.

XX A mutein (AAR92012) of tissue factor pathway inhibitor (TFPI)

CC is prep'd. by site-directed mutagenesis of an encoding sequence.
 CC in the muten, the lysine residue in the PI reactive site of the
 CC first Kunitz-type domain of TFPI is replaced by arginine. This
 CC domain is required for the inhibition of Factor-VIIIa/tissue
 CC factor (TF) complex. The muten may be expressed in Saccharomyces
 CC cerevisiae transformants, esp. as a ubiquitin fusion protein,
 CC and as a Factor-VIIIa/TF/Xa binding protein.
 XX
 SQ Sequence 276 AA;

Query/Match 100.0%; Score 96; DB 17; Length 276;
 Best Local Similarity 100.0%; Pred. No. 8.3e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DSEDEHHTITDTPLP 18
 1 dseedehtitdtelp 18

RESULT 11

AAM30311
 ID AAM30311 standard; protein: 276 AA.

AC AAM30311;

DT 30-JAN-1998 (first entry)

DE Recombinant non-glycosylated TFPI.

XX Tissue factor pathway inhibitor; TFPI; human; tissue factor inhibitor;
 KM lipoprotein-associated coagulation inhibitor; coagulation inhibitor; TFPI;
 KM LACI; extrinsic pathway inhibitor; protein refolding; clot-inhibitor;
 KM protein solubility modification; EPI.
 XX
 OS Homo sapiens.

XX

XX Key Location/Qualifiers

FT Modified-site 2 /note- "phosphorylated to varying degrees, but does not
 FT affect TFPI function"

FT Disulfide-bond 26..76
 FT Disulfide-bond 35..59
 FT Disulfide-bond 51..72
 FT Disulfide-bond 97..147
 FT Disulfide-bond 106..130
 FT Disulfide-bond 122..143
 FT Disulfide-bond 189..239
 FT Disulfide-bond 198..232
 FT Disulfide-bond 214..235

XX

XX W09640784-A2.

XX

XX 19-DEC-1996.

XX

XX 07-JUN-1996; 96MO-US09980.

XX

XX 07-JUN-1995; 95US-0477677.

XX

XX 07-JUN-1995; 95US-0473668.

XX

XX (CHIR) CHIRON CORP.

XX (SEAR) SEARLE & CO G D.

XX

XX Arve BH, Bild GS, Chen B, Dorlin GT, Gustafson ME;

XX Hailenbeck RF, Hora MS, Johnson GV, Johnson K, Madani H;

XX Pattison GL, Rana RK, Tsang M;

XX

XX WPI; 1997-087056/08.

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FT Disulfide-bond 214..235
 FT Modified-site 228 /note- "N-glycosylated"
 XX
 XX WO9834634-A1.
 XX
 PD 13-AUG-1998.
 XX
 PF 06-FEB-1998; .98WO-0502699.
 XX
 PR 06-FEB-1997; 97US-0796850.
 XX
 PA (ENTR-) ENTREMED INC.
 PI Green ~~Pat~~ Papathanassiou AE;
 XX
 DR WPI; 1998-446947/38.
 XX
 PT Composition comprising tissue factor pathway inhibitor for
 PT inhibiting cell proliferation - for treating angiogenesis related
 PT diseases e.g. cancer, arthritis, macular degeneration and diabetic
 PT retinopathy
 PS
 CC Claim 6; Pages 23-24; 37pp; English.
 XX
 CC The present sequence represents the human tissue factor pathway
 CC inhibitor (TFPI). The invention provides compositions using TFPI
 CC and its homologs, e.g. TFPI-2 (AA66136), for inhibiting cell
 CC proliferation. The compositions are claimed to be useful for inhibiting
 CC an angiogenesis-related disease, such as cancer, arthritis, macular
 CC degeneration or diabetic retinopathy.
 XX
 SQ Sequence 276 AA:
 XX

Query Match 100.0%; Score 96; DB 19; Length 276;
 Best Local Similarity 100.0%; Pred. No. 8.3e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 DSEDEDEHTTTTDELP 18
 DB 1 dseedehtlttdelp 18

RESULT 13
 AAR37312
 ID AAR37312 standard; protein; 277 AA.
 XX
 AC AAR37312;
 XX
 DT 20-SEP-1993 (first entry)
 XX
 DE Non-glycosylated TFPI.
 XX
 DE Non-glycosylated TFPI.
 XX
 KW Non-glycosylated; tissue factor pathway inhibitor; TFPI; multivalent;
 KW lipoprotein associated coagulation inhibitor; inhibitor; Kunitz-type;
 KW coagulation; domain; factor VIIa; LACI; tissue factor; factor Xa;
 KW complex; coagulation.
 XX
 OS Escherichia coli.
 XX
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 26..76
 FT Disulfide-bond 51..72
 FT Disulfide-bond 97..147
 FT Disulfide-bond 106..130
 FT Disulfide-bond 122..143
 FT Disulfide-bond 189..239
 FT Disulfide-bond 196..222
 FT Disulfide-bond 214..235
 XX
 PN US212091-A.
 XX

PD 18-MAY-1993.
 XX
 PF 02-MAR-1992; 92US-0844297.
 XX
 PR 02-MAR-1992; 92US-0844297.
 XX
 PA (MONS) MONSANTO CO.
 PI Diaz-Collmer JA, Gustafson ME, Mun T;
 XX
 DR WPI; 1993-175458/21.
 XX
 PT Prod. of non-glycosylated form of tissue factor pathway
 PT inhibitor in high yield - comprises culturing E.coli cells
 PT transformed with replication expression vector and subjecting
 PT isolated inclusion bodies to subpilotolysis or redn. with
 PT beta-mercapto-ethanol, etc.
 XX
 PS Claim 1; Column 15-18; 25pp; English.
 XX
 CC This sequence represents a non-glycosylated form of tissue factor
 CC pathway inhibitor (TFPI). TFPI is alternatively known as lipo-
 CC protein associated coagulation inhibitor (LACI). TFPI is a multi-
 CC valent Kunitz-type inhibitor of coagulation. The primary amino acid
 CC sequence of TFPI shows that it contains a highly negatively charged
 CC amino terminus, three tandem Kunitz-type inhibitory domains and a
 CC highly positively charged carboxyl terminal. The first Kunitz domain
 CC of TFPI is needed for the inhibition of factor VIIa/tissue factor
 CC complex and the second Kunitz domain of TFPI is responsible for the
 CC inhibition of factor Xa. The function of the third Kunitz domain
 CC is unknown. TFPI is thought to act in vivo to limit the initiation
 CC of coagulation by forming an inert, quaternary factor Xa:TFPI:factor
 CC VIIa:tissue factor complex.
 XX
 SQ Sequence 277 AA:
 XX

Query Match 100.0%; Score 96; DB 14; Length 277;
 Best Local Similarity 100.0%; Pred. No. 8.3e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 DSEDEDEHTTTTDELP 18
 DB 2 dseedehtlttdelp 19

RESULT 14
 AAP92002
 ID AAP92002 standard; protein; 304 AA.
 XX
 AC AAP92002;
 XX
 DT 09-FEB-1990 (first entry)
 XX
 DE Human tissue factor inhibitor (TFI).
 XX
 DE Human tissue factor inhibitor (TFI).
 XX
 KW Human tissue factor inhibitor; TFI; human placenta lambda-P9 clone; basic
 KW protease inhibitor gene superfamily
 KW
 XX
 OS Homo sapiens.
 XX
 XX
 FH Key Location/Qualifiers
 FT Region 1..28
 FT /label- "Signal-region"
 FT /note- "A-T rich"
 FT Cleavage-site 28..29
 FT /note- "Possible site for signal peptidase"
 FT Protein 29..304
 FT Region 145..147
 FT Region 195..197
 FT /note- "Potential N-linked glycosylation site"
 FT /note- "Potential N-linked glycosylation site"
 FT Region 256..258.
 XX

FT /note- "Potential N-linked glycosylation site"
 FT 31..53
 FT /note- "See comments below"
 FT 82..88
 FT /note- "See comments below"
 FT 153..16
 FT /note- "See comments below"
 XX
 XX EP318451-A
 XX PN
 XX PD: 31 MAY 1989
 XX
 XX 22-JUL-1988; 88EP-0870127.
 XX
 XX 23-NOV-1987; 87US-0123753.
 XX
 XX (MONS) MONSANTO CO (UNIW).
 XX
 XX Broze GJ, Kretzmer KK, Wun TC;
 XX PI
 XX WPI; 1989-159483/22.
 XX DR
 XX N-PSDB; AAN90108.
 XX
 XX DNA encoding human tissue factor inhibitor
 FT - used in study of coagulation cascade for agents
 FT which inhibit factor Xa and Factor VIIA-TF
 XX
 XX Claim 3; Figure 3; 14pp; English.
 XX
 XX Amino acid sequence of tissue factor inhibitor (TFI) cDNA isolate from
 CC lambda-p9 clone of human placenta cDNA library. Domains discerned
 CC include: highly negatively charged N-terminal; highly positively charged
 CC carboxy-terminal; intervening portion consisting of 3 homologous domains
 CC with sequences typical of Kunitz-type enzyme inhibitors. Based on
 CC homology study, it appears to be a member of the basic protease
 CC inhibitor gene superfamily. Sequences in misc. regions in feature table
 CC above have been independently confirmed by amino acid sequence analysis.
 XX
 XX Sequence 304 AA;
 SQ
 Query Match 100.0%; Score 96; DB 10; Length 304;
 Best Local Similarity 100.0%; Pred. No. 9.2e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DSEDEEHTIITDTLPP 18
 DB 29 dseedehtitdtelpp 46
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 RESULT 15
 AAR81884
 ID AAR81884 standard; protein; 304 AA.
 XX
 XX AAR81884;
 AC
 XX
 XX 18-MAR-1996 (first entry)
 DT
 XX
 XX Lipoprotein-associated coagulation inhibitor (LACI).
 DE
 XX
 XX Lipoprotein-associated coagulation inhibitor; LACI; kallikrein;
 KW inhibitor; KIP; Kunitz domain; hereditary angioedema.
 XX
 XX Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 FH Peptide 1..28
 FT /label- sig_peptide
 FT 50..107
 FT Domain /note- "Kunitz domain LACI-K1"
 FT 121..178
 FT Domain /note- "Kunitz domain LACI-K2"
 FT 213..270
 FT Domain

FT /note- "Kunitz domain LACI-K3"
 XX WO9521601-A2.
 XX PN
 XX 17-AUG-1995.
 PD
 XX
 XX 11-JAN-1995; 95WO-US00299.
 XX
 XX 10-MAR-1994; 94US-0208264.
 PR
 XX 11-JAN-1994; 94US-0179964.
 PR
 XX (PROT-) PROTEIN ENG CORP.
 PA
 XX Ladner RC, Markland W;
 XX PI
 XX WPI; 1995-292934/38.
 DR
 XX
 XX Kallikrein inhibiting proteins comprising a Kunitz domain homologous
 FT to bovine pancreatic trypsin inhibitor - useful for preventing or
 FT treating disorders attributable to excessive kallikrein activity.
 FT eg. in hereditary angioedema.
 XX
 XX Disclosure; Page 24; 46pp; English.
 PS
 XX AAR81884 is the human lipoprotein-associated coagulation inhibitor
 CC LACI. The Kunitz domain, LACI-K1, of LACI is a kallikrein
 CC inhibiting protein (KIP) upon which the claimed KIPs of the invention
 CC are based. The KIPs can be used for treating or preventing disorders
 CC attributable to excessive kallikrein activity, e.g. hereditary
 CC angioedema. The KIPs can also be used for assaying, purifying and in
 CC vivo imaging of kallikrein.
 XX
 XX Sequence 304 AA;
 SQ
 Query Match 100.0%; Score 96; DB 16; Length 304;
 Best Local Similarity 100.0%; Pred. No. 9.2e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DSEDEEHTIITDTLPP 18
 DB 29 dseedehtitdtelpp 46
 |||||

Search completed: September 20, 2002, 10:28:38
 Job time: 81 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 20, 2002, 10:27:17 ; Search time 12.96 Seconds

(Without alignments)
33.924 Million cell updates/sec

Title: US-08-854-764-7

Sequence: 1 DSEDEDETTITDRLFP 18

Scoring table: BLOSUM62

Searched: GAPOP 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/prodata/2/1aa/5A.COMB.pep.*
2: /cgn2_6/prodata/2/1aa/5B.COMB.pep.*
3: /cgn2_6/prodata/2/1aa/6A.COMB.pep.*
4: /cgn2_6/prodata/2/1aa/6B.COMB.pep.*
5: /cgn2_6/prodata/2/1aa/PCUS.COMB.pep.*
6: /cgn2_6/prodata/2/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	96	100.0	18	3	US-08-854-764-7
2	96	100.0	18	5	PCT-US95-09377-7
3	96	100.0	161	1	US-08-437-841-19
4	96	100.0	161	1	US-08-286-521-19
5	96	100.0	161	1	US-08-436-175-19
6	96	100.0	161	1	US-08-943-682-19
7	96	100.0	161	5	PCT-US95-09464-19
8	96	100.0	189	1	US-07-828-920A-7
9	96	100.0	276	1	US-07-828-920A-1
10	96	100.0	276	1	US-08-437-841-9
11	96	100.0	276	1	US-08-286-521-9
12	96	100.0	276	1	US-08-436-175-9
13	96	100.0	276	2	US-08-796-850-1
14	96	100.0	276	3	US-08-854-764-3
15	96	100.0	276	4	US-08-943-682-9
16	96	100.0	276	4	PCT-US95-09377-3
17	96	100.0	276	5	PCT-US95-09464-9
18	96	100.0	277	1	US-07-844-297-1
19	96	100.0	304	1	US-08-026-145-2
20	96	100.0	304	1	US-08-446-646-9
21	96	100.0	304	1	US-08-676-125A-18
22	96	100.0	304	2	US-09-136-012A-18
23	96	100.0	304	3	US-08-676-124-1
24	96	100.0	304	3	US-08-208-264A-25
25	96	100.0	304	3	US-09-414-878-1
26	96	100.0	304	3	US-09-240-136-1
27	96	100.0	304	4	US-09-054-782-2

28	96	100.0	304	4	US-09-421-097-25	Sequence 25, Appl
29	96	100.0	304	3	US-08-854-764-2	Patent No. 546783
30	96	100.0	352	3	PCT-US95-09377-2	Sequence 2, Appl
31	96	100.0	352	5	PCT-US95-09377-2	Sequence 2, Appl
32	86	89.6	27	6	546783-26	Patent No. 546783
33	50.5	52.6	224	3	US-08-630-916A-50	Sequence 50, Appl
34	48	50.0	22	6	5427926-1	Patent No. 542796
35	48	50.0	1085	1	US-08-431-080-28	Sequence 28, Appl
36	48	50.0	1085	2	US-08-938-534-28	Sequence 18, Appl
37	47	49.0	1189	3	US-09-195-868-15	Sequence 28, Appl
38	47	49.0	1229	3	US-09-195-868-15	Sequence 153, App
39	46	47.9	48	4	US-09-314-268-153	Sequence 2, Appl
40	45	46.9	570	3	US-08-826-246-2	Sequence 2, Appl
41	45	46.9	570	3	US-08-944-495-2	Sequence 2, Appl
42	45	46.9	570	3	US-09-126-640-7	Sequence 2, Appl
43	45	46.9	570	4	US-08-925-588-2	Sequence 7, Appl
44	45	46.9	570	4	US-09-288-292A-7	Sequence 7, Appl
45	44	45.8	504	1	US-08-457-274A-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1
US-08-854-764-7
Sequence 7, Application US/08854764
Patent No. 6103500
GENERAL INFORMATION:
APPLICANT: Innes, Michael
TITLE OF INVENTION: Production of Tissue Factor Pathway
TITLE OF INVENTION: Inhibitor
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton St.
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.308
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,764
FILING DATE: 12-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/286,530
FILING DATE: 05-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Saveriede, Paul B.
REGISTRATION NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 0991.001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2585
TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO.: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-854-764-7
Query Match 100.0%; Score 96; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 2, 1e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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3
RESULT 05-08-437-841-19
; Sequence 19, Application US/08437841
; Patent No. 5563123
; GENERAL INFORMATION:
; APPLICANT: Innis, Michael
; APPLICANT: Creasey, Abba
; TITLE OF INVENTION: Chimeric Proteins
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton St.
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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ZIP: 34000
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30B
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/286,521
 FILING DATE: 05-AUG-1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Saveriede, Paul B.
 REGISTRATION NUMBER: 36,914
 REFERENCE/DOCKET NUMBER: 0990.001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 510-601-2585
 TELEFAX: 510-655-3542
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 161 amino acids
 TYPE: amino acid
 STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-286-521-19

Query Match. 100.0%; Score 96; DB 1; Length 161;
Best Local Similarity 100.0%; Pred. No. 2.3e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DSEDEEHITITDTELP 18
|||||
DB 1 DSEDEEHITITDTELP 18

RESULT 5
US-08-436-175-19
Sequence 19, Application US/08436175
Patent No. 5696088

GENERAL INFORMATION:

APPLICANT: Innis, Michael
APPLICANT: Creasey, Abia
TITLE OF INVENTION: Chimeric Proteins
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton St.
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,175
FILING DATE: 09-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,521
FILING DATE: 05-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Saveriede, Paul B.
REGISTRATION NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 0990.001
TELEPHONE: 510-601-2585
TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 161 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-436-175-19

Query Match 100.0%; Score 96; DB 1; Length 161;
Best Local Similarity 100.0%; Pred. No. 2.3e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DSEDEEHITITDTELP 18
|||||
DB 1 DSEDEEHITITDTELP 18

RESULT 6
US-08-943-682-19
Sequence 19, Application US/08943682
Patent No. 6174721
GENERAL INFORMATION:

APPLICANT: Innis, Michael
APPLICANT: Creasey, Abia
TITLE OF INVENTION: Chimeric Proteins
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton St.
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,682
FILING DATE: 03-OCT-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/438,184
FILING DATE: 09-MAY-1995
APPLICATION NUMBER: US 08/286,521
FILING DATE: 05-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Saveriede, Paul B.
REGISTRATION NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 0990.001
TELEPHONE: 510-601-2585
TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 161 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-943-682-19

Query Match 100.0%; Score 96; DB 4; Length 161;
Best Local Similarity 100.0%; Pred. No. 2.3e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DSEDEEHITITDTELP 18
|||||
DB 1 DSEDEEHITITDTELP 18

RESULT 7
PCT-US95-09464-19
Sequence 19, Application PC/TUS9509464

GENERAL INFORMATION:

APPLICANT: CHIRON CORPORATION
TITLE OF INVENTION: Chimeric Proteins
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton St.
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/09464
FILING DATE: 25-JULY-1995

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Saweigle, Paul B.
REGISTRATION NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 0990.100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2585
TELEFAX: 510-635-3542
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 161 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US95-09460-19

Query Match 100.0%; Score 96; DB 5; Length 161;
Best Local Similarity 100.0%; Pred. No. 2.3e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSEDEEHTIITDTELP 18
DB 1 DSEDEEHTIITDTELP 18

RESULT 8

US-07-828-920A-7
Sequence 7, Application US/07828920A
Patent No. 5312736
GENERAL INFORMATION:
APPLICANT: Rasmussen, Jesper
APPLICANT: No. 5312736dfang, Ole Juul
TITLE OF INVENTION: Anticoagulant Protein
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5312736o No. 5312736disk of No. 5312736th America, Inc.
STREET: 405 Lexington Avenue, Suite 6200
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/828, 920A
FILING DATE: 19920127
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 4080/89
FILING DATE: 18-AUG-1989
APPLICATION NUMBER: WO PCT/DK90/00212
FILING DATE: 17/AUG/1990
ATTORNEY/AGENT INFORMATION:
NAME: Zelson, Steve T.
REGISTRATION NUMBER: 30335
REFERENCE/DOCKET NUMBER: 3287.204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 189 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-828-920A-7

Query Match 100.0%; Score 96; DB 1; Length 189;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSEDEEHTIITDTELP 18
DB 29 DSEDEEHTIITDTELP 46

RESULT 9

US-07-828-920A-1
Sequence 1, Application US/07828920A
Patent No. 5312736
GENERAL INFORMATION:
APPLICANT: Rasmussen, Jesper
APPLICANT: No. 5312736dfang, Ole Juul
TITLE OF INVENTION: Anticoagulant Protein
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5312736o No. 5312736disk of No. 5312736th America, Inc.
STREET: 405 Lexington Avenue, Suite 6200
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/828, 920A
FILING DATE: 19920127
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 4080/89
FILING DATE: 18-AUG-1989
APPLICATION NUMBER: WO PCT/DK90/00212
FILING DATE: 17/AUG/1990
ATTORNEY/AGENT INFORMATION:
NAME: Zelson, Steve T.
REGISTRATION NUMBER: 30335
REFERENCE/DOCKET NUMBER: 3287.204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 276 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE: Homo sapiens
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: Protein
LOCATION: 1..276
US-07-828-920A-1

Query Match 100.0%; Score 96; DB 1; Length 276;
Best Local Similarity 100.0%; Pred. No. 4.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSEDEEHTIITDTELP 18
DB 1 DSEDEEHTIITDTELP 18

RESULT 10

US-08-437-841-9
Sequence 9, Application US/08437841

Patent No. 5563123
GENERAL INFORMATION:
APPLICANT: Innis, Michael
TITLE OF INVENTION: Chimeric Proteins
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton St.
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,841
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/286,521
FILING DATE: 05-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Saveriede, Paul B.
REGISTRATION NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 0990.001
TELEPHONE: 510-601-2585
TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 276 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-437-841-9

Query Match 100.0%; Score 96; DB 1; Length 276;
Best Local Similarity 100.0%; Pred. No. 4,1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DSEDEEHITITDTELP 18
Db 1 DSEDEEHITITDTELP 18

RESULT 11
US-08-286-521-9
Sequence 9, Application US/08286521
Patent No. 5589359
GENERAL INFORMATION:
APPLICANT: Innis, Michael
TITLE OF INVENTION: Chimeric Proteins
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton St.
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/286,521
FILING DATE: 05-AUG-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Saveriede, Paul B.
REGISTRATION NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 0990.001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2585
TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 276 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-286-521-9

Query Match 100.0%; Score 96; DB 1; Length 276;
Best Local Similarity 100.0%; Pred. No. 4,1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DSEDEEHITITDTELP 18
Db 1 DSEDEEHITITDTELP 18

RESULT 12
US-08-436-175-9
Sequence 9, Application US/08436175
Patent No. 5696088
GENERAL INFORMATION:
APPLICANT: Innis, Michael
TITLE OF INVENTION: Chimeric Proteins
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton St.
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,175
FILING DATE: 09-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,521
FILING DATE: 05-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Saveriede, Paul B.
REGISTRATION NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 0990.001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2585
TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 276 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-436-175-9

Query Match 100.0%; Score 96; DB 1; Length 276;
Best Local Similarity 100.0%; Pred. No. 4.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSEDEEHTIITDTELP 18
DB 1 DSEDEEHTIITDTELP 18

RESULT 13

US-08-796-850-1

; Sequence 1, Application US/08796850

; Patent No. 5981471

; GENERAL INFORMATION:

; APPLICANT: Papathanassiou, Adonia E

; APPLICANT: Green, Shawn J.

; TITLE OF INVENTION: Compositions and Methods for Inhibiting

; TITLE OF INVENTION: Cellular Proliferation

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Jones & Askew

; STREET: 191 Peachtree Street, 37th Floor

; CITY: Atlanta

; STATE: Georgia

; COUNTRY: U.S.A.

; ZIP: 30303

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk.

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/796,850

; FILING DATE:

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Greene, Jamie L.

; REGISTRATION NUMBER: 32,467

; REFERENCE/DOCKET NUMBER: 05213-0290

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (404) 818-3700

; TELEFAX: (404) 818-3799

; INFORMATION FOR SEQ ID NO: 1:

; LENGTH: 276 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: N-terminal

; ORIGINAL SOURCE:

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: Active-site

; LOCATION: 2..3

; OTHER INFORMATION: /note= "Site of partial

; OTHER INFORMATION: phosphorylation"

; FEATURE:

; NAME/KEY: Active-site

; LOCATION: 117..118

; OTHER INFORMATION: /note= "Potential site for N-linked

; OTHER INFORMATION: glycosylation"

; FEATURE:

; NAME/KEY: Active-site

; LOCATION: 167..168

; OTHER INFORMATION: /note= "Potential site for N-linked

; OTHER INFORMATION: glycosylation"

; FEATURE:

; NAME/KEY: Active-site

; LOCATION: 228..229

; OTHER INFORMATION: /note= "Potential site for N-linked

; FEATURE: glycosylation"

; NAME/KEY: Domain

; LOCATION: 26..76

; OTHER INFORMATION: /label= Kunitz-1

; FEATURE:

; NAME/KEY: Domain

; LOCATION: 97..147

; OTHER INFORMATION: /label= Kunitz-2

; FEATURE:

; NAME/KEY: Domain

; LOCATION: 189..239

; OTHER INFORMATION: /label= Kunitz-3

US-08-796-850-1

Query Match

Best Local Similarity 100.0%; Score 96; DB 2; Length 276;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSEDEEHTIITDTELP 18

DB 1 DSEDEEHTIITDTELP 18

RESULT 14

US-08-854-764-3

; Sequence 3, Application US/08854764

; Patent No. 6103500

; GENERAL INFORMATION:

; APPLICANT: Innes, Michael

; TITLE OF INVENTION: Production of Tissue Factor Pathway

; TITLE OF INVENTION: Inhibitor

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Chiron Corporation

; STREET: 4560 Horton St.

; CITY: Emeryville

; STATE: CA

; COUNTRY: USA

; ZIP: 94608

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.30B

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/854,764

; FILING DATE: 12-MAY-1997

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/286,530

; FILING DATE: 05-AUG-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Savereide, Paul B.

; REGISTRATION NUMBER: 36,914

; REFERENCE/DOCKET NUMBER: 0991.001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 510-601-2585

; TELEFAX: 510-655-3542

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 276 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-854-764-3

Query Match

100.0%; Score 96; DB 3; Length 276;

Best Local Similarity 100.0%; Pred. No. 4.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DSEDEHHTITDTLPP 18
| | | | | | | | | | | | | | | | | |
Db 1 DSEDEHHTITDTLPP 18

RESULT 15

US-08-943-682-9
Sequence 9, Application US/08943682
Patent No. 6174721
GENERAL INFORMATION:
APPLICANT: Innis, Michael
APPLICANT: Creasey, Abba
TITLE OF INVENTION: Chimeric Proteins
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton St.
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentlin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,682
FILING DATE: 03-OCT-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/438,184
FILING DATE: 09-MAY-1995
APPLICATION NUMBER: US 08/286,521
FILING DATE: 05-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Savereide, Paul B.
REGISTRATION NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 0990.001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2585
TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 276 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-943-682-9

Query Match 100.0%; Score 96; DB 4; length 276;

Best Local Similarity 100.0%; Pred. No. 4.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DSEDEHHTITDTLPP 18
| | | | | | | | | | | | | | | | | |
Db 1 DSEDEHHTITDTLPP 18

Search completed: September 20, 2002, 10:27:39
Job time: 22 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 20, 2002, 10:27:17 ; Search time 14.76 Seconds

(without alignments)
117.182 Million cell updates/sec

Title: US-08-854-764-7

Sequence: 1 DSEDEDEHITITPTELP 18

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	96	100.0	304	1	TIHUGK
2	90	92.8	304	1	JC2264
3	56	58.3	1770	2	S56221
4	55	57.3	2225	2	T26063
5	51	53.1	873	2	JC4863
6	51	53.1	873	2	JC7079
7	50.5	52.6	1256	2	JE0209
8	49	51.0	590	2	A40437
9	48	50.0	1085	2	S55352
10	47.5	49.5	1221	2	A49457
11	47	49.0	300	2	SI2143
12	47	49.0	360	2	S69063
13	46	47.9	572	2	AD1209
14	46	47.9	2670	2	A46719
15	45	46.9	244	2	T20784
16	45	46.9	259	1	B70314
17	45	46.9	354	2	I48722
18	45	46.9	404	2	G86536
19	45	46.9	404	2	A72087
20	45	46.9	455	2	I48724
21	45	46.9	599	2	T24333
22	44.5	46.4	471	2	T21972
23	44	45.8	106	2	T04032
24	44	45.8	306	2	JC7687
25	44	45.8	379	2	E69824
26	44	45.8	502	2	JX0334
27	44	45.8	504	2	A22631
28	44	45.8	888	2	A55318
29	44	45.8	888	2	JC5399

ALIGNMENTS

30 44 45.8 1401 2 T48079
31 44 45.8 2175 1 S03170
32 43.5 45.3 552 2 T27427
33 43.5 45.3 1188 2 JC4889
34 43 44.8 239 2 S68257
35 43 44.8 449 2 D69037
36 43 44.8 489 2 A31555
37 43 44.8 515 2 A43289
38 43 44.8 699 2 S25541
39 43 44.8 1038 1 JC5757
40 43 44.8 1038 1 T18222
41 43 44.8 1054 2 T30901
42 43 44.8 1105 1 S40243
43 43 44.8 1106 1 A39299
44 43 44.8 1107 1 A41618
45 43 44.8 1217 2 A45493

hypotheical prote
homeotic protein c
hypotheical prote
phosphatidylinosit
phospholipase C (E
PERT112-like protei
interferon gamma r
CDC4L protein - hu
heat shock protein
DNA-directed DNA p
DNA polymerase del
cyclic nucleotide
DNA-directed DNA p
DNA-directed DNA p
DNA-directed DNA p
phospholipase C-be

RESULT 1
TIHUGK
tissue factor pathway inhibitor precursor [validated] - human
N:Alternate names: extrinsic pathway inhibitor; lipoprotein-associated coagulation in
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence-revision 30-Jun-1992 #text-change 08-Dec-2000
C:Accession: A23712; A39176; A28650; A60433; S13034; A3315; A28294; S03903
R:Girard, T.J.; Eddy, R.; Weselohschmidt, R.L.; Macphail, L.A.; Likert, R.M.; Byers, M
J. Biol. Chem. 266, 5036-5041, 1991
A:Title: Structure of the human lipoprotein-associated coagulation inhibitor gene. In
A:Reference number: A23712; MUID:91161553
A:Accession: A23712
A:Molecule type: DNA
A:Residues: 1-304 <GIR>
A:Cross-references: GB:M59493; GB:M59499; NID:9187204; PIDN:AAA59526.1; PID:9187206
R:van der Logt, C.P.E.; Reitsma, P.H.; Bertina, R.M.
Biochemistry 30, 1571-1577, 1991
A:Title: Intron-exon organization of the human gene coding for the lipoprotein-assoc
A:Reference number: A39176; MUID:91129227
A:Accession: A39176
A:Molecule type: DNA
A:Residues: 1-304 <VAN>
A:Cross-references: GB:M58650; GB:J05312; NID:9186827; PIDN:AAA59480.1; PID:9186829.
R:Hu, T.C.; Kretzmer, K.K.; Girard, T.J.; Miletich, J.P.; Broze Jr., G.J.
J. Biol. Chem. 263, 6001-6004, 1988
A:Title: Cloning and characterization of a cDNA coding for the lipoprotein-associated
A:Reference number: A28650; MUID:88198127
A:Accession: A28650
A:Molecule type: mRNA
A:Residues: 1-304 <MUN>
A:Cross-references: GB:J03225; NID:9180545; PIDN:AAA52022.1; PID:9180546
A:Note: part of this sequence, including the amino end of the mature protein, was con
R:Girard, T.J.; Warren, L.A.; Novotny, W.F.; Bejcek, B.E.; Miletich, J.P.; Broze Jr.,
Thromb. Res. 55, 37-50, 1989
A:Title: Identification of the 1.4 kb and 4.0 kb messages for the lipoprotein associa
A:Reference number: A60433; MUID:89388722
A:Accession: A60433
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-304 <G12>
A:Experimental source: endothelial cells
A:Accession: B60433
A:Molecule type: protein
A:Residues: 'xx', 31-53, 'x', 55-56 <G13>
A:Experimental source: recombinant material from mouse C137 cells
R:Girard, T.J.; McCourt, D.; Novotny, W.F.; Macphail, L.A.; Likert, R.M.; Broze Jr.,
Biochem. J. 270, 621-625, 1990
A:Title: Endogenous phosphorylation of the lipoprotein-associated coagulation inhibit
A:Reference number: S13034; MUID:91054349
A:Accession: S13034
A:Molecule type: protein
A:Residues: 29-35 <G14>

R:Novotny, W.F.; Girard, T.J.; Miletich, J.P.; Broze Jr., G.J.
 J. Biol. Chem. 264, 18832-18837, 1989
 A:Title: Purification and characterization of the lipoprotein-associated coagulation inhibitor
 A:Reference number: A34315; MUID:90036996
 A:Accession: A34315
 A:Molecule type: protein
 A:Residues: 'XX', 31-33, 'L', 35-50 <NOV>
 A:Experimental source: plasma
 R:Pedersen, A.H.; Nordfang, O.; Norris, F.; Christensen, P.M.; Moeller, K.
 J. Biol. Chem. 265, 16786-16793, 1990
 A:Title: Recombinant human extrinsic pathway inhibitor. Production, isolation, and characterization
 A:Reference number: A38294; MUID:91009092
 A:Accession: A38294
 A:Molecule type: protein
 A:Residues: 29-51 <PED>
 R:Girard, T.J.; Warren, L.A.; Novotny, W.F.; Likert, K.M.; Brown, S.G.; Miletich, J.P.;
 Nature 338, 518-520, 1989
 A:Title: Functional significance of the Kunitz-type inhibitory domains of lipoprotein-associated
 A:Reference number: S03903; MUID:89181950
 A:Contents: annotation; site-directed mutagenesis
 C:Comment: The first Kunitz-type domain binds the factor VIIa/tissue factor complex; the
 C:Genetics:
 A:Gene: GDB:TFPI
 A:Cross-references: GDB:127364; OMIM:152310
 A:Map position: 2q32-2q32
 A:Introns: 41/1; 107/1; 120/1; 179/1; 210/1; 270/1
 C:Function:
 A:Description: regulates clotting by factor Xa-dependent inhibition of the coagulation factor
 C:Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor
 C:Keywords: anticoagulant; blood coagulation; duplication; glycoprotein; heparin binding
 F:1-28/Domain: signal sequence #status predicted <SIG>
 F:29-304/Product: tissue factor pathway inhibitor #status experimental <MAP>
 F:125-175/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
 F:54-104/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
 F:217-267/Domain: animal Kunitz-type proteinase inhibitor homology <BP3>
 F:30/Binding site: phosphate (Ser) (covalent) #status experimental
 F:284-289/Region: heparin binding #status predicted
 F:54-104, 63-87, 79-100, 125-175, 134-158, 150-171, 217-267, 226-250, 242-263/disulfide bonds: #
 F:64/Inhibitory site: Lys (coagulation factor VII/tissue factor complex) #status experimental
 F:135/Inhibitory site: Arg (coagulation factor X) #status predicted
 F:145,195,256/Binding site: carboxylate (Asn) (covalent) #status predicted
 F:227/Inhibitory site: Arg (unidentified proteinase) #status predicted

Query Match 100.0%; Score 96; DB 1; Length 304;
 Best Local Similarity 100.0%; Pred. No. 2.7e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSEDEEHTIITDELPP 18
 |||||
 DB 29 DSEDEEHTIITDELPP 46

RESULT 2
 JC2264
 tissue factor pathway inhibitor precursor - rhesus macaque
 N:Alternate names: extrinsic pathway inhibitor; lipoprotein-associated coagulation inhibitor
 C:Species: Macaca mulatta (rhesus macaque)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
 C:Accession: JC2264
 R:Kamel, S.; Kamikubo, Y.; Hamuro, T.; Fujimoto, H.; Ishihara, M.; Yonemura, H.; Miyamoto
 J. Biochem. 115, 708-714, 1994
 A:Title: Amino acid sequence and inhibitory activity of rhesus monkey tissue factor path
 A:Reference number: JC2264; MUID:94375417
 A:Accession: JC2264
 A:Molecule type: mRNA
 A:Residues: 1-304 <KAM>
 A:Cross-references: GB:S73337; NID:g685016; PIDN:RAB31955.1; PID:g685017
 A:Experimental source: liver
 C:Comment: This protein inhibits the activities of factor Xa and tissue factor-factor VI
 C:Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor
 C:Keywords: anticoagulant; glycoprotein; serine proteinase inhibitor

F:1-28/Domain: signal sequence #status predicted <SIG>
 F:29-304/Product: tissue factor pathway inhibitor #status predicted <MAP>
 F:54-104/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
 F:125-175/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
 F:217-267/Domain: animal Kunitz-type proteinase inhibitor homology <BP3>
 F:54-104, 63-87, 79-100, 125-175, 134-158, 150-171, 217-267, 226-250, 242-263/disulfide bonds
 F:64/Inhibitory site: Lys (coagulation factor VII/tissue factor complex) #status pred
 F:135/Inhibitory site: Arg (coagulation factor X) #status predicted
 F:145,195,256/Binding site: carboxylate (Asn) (covalent) #status predicted
 F:227/Inhibitory site: Arg (unidentified proteinase) #status predicted

Query Match 93.8%; Score 90; DB 1; Length 304;
 Best Local Similarity 94.4%; Pred. No. 2.3e-06;
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSEDEEHTIITDELPP 18
 |||||
 DB 29 DSEDEEHTIITDELPP 46

RESULT 3
 SS6221
 hypothetical protein YFL033c - yeast (Saccharomyces cerevisiae)
 C:Species: Saccharomyces cerevisiae
 C:Date: 02-Sep-1995 #sequence_revision 19-Oct-1995 #text_change 29-Oct-1999
 C:Accession: S56221
 R:Murakami, Y.; Naitou, M.; Hagiwara, H.; Shibata, T.; Ozawa, M.; Sasanuma, S.I.; Sas
 submitted to the EMBL Data Library, May 1995
 A:Description: Analysis of the nucleotide sequence of chromosome VI from Saccharomyces
 A:Reference number: S56186
 A:Accession: S56221
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1770 <MUR>
 A:Cross-references: EMBL:D50617; NID:g836685; PIDN:BAA09206.1; PID:dl009846; PID:g836
 C:Genetics:
 A:Gene: SGD:RIM15
 A:Cross-references: SGD:S0001861; MIPS:YFL033c
 A:Map position: 6L

Query Match 58.3%; Score 56; DB 2; Length 1770;
 Best Local Similarity 64.3%; Pred. No. 3.6;
 Matches 9; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 2 SEDEEHTIITDELPP 15
 |||||
 DB 1754 SQDEEHTILSDSD 1767

RESULT 4
 T26063
 hypothetical protein W01F3.3 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T26063
 R:Cummings, P.
 submitted to the EMBL Data Library, March 1997
 A:Reference number: Z20145
 A:Accession: T26063
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-2225 <WIL>
 A:Cross-references: EMBL:X92815; PIDN:CAB07294.1; GSPDB:GN00023; CESP:W01F3.3
 C:Experimental source: clone W01F3
 C:Genetics:
 A:Gene: CESP:W01F3.3
 A:Map position: 5
 A:Introns: 33/1; 56/1; 100/1; 142/3; 271/3; 451/1; 525/3; 774/1; 1093/1; 1178/1; 1221

Query Match 57.3%; Score 55; DB 2; Length 2225;

Best Local Similarity 55.6%; Pred. No. 6.7;
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 DSEDEEHITITDTELP 18
DB 663 ETEDEEHAVPTTPIAP 680

RESULT 5

JC4863
homeobox protein zhx-1 - mouse
N:Alternate names: homeodomain-containing protein zhx-1
C:Species: Mus musculus (house mouse)
C>Date: 15-Aug-1996 #sequence_revision 18-Oct-1996 #text_change 21-Jul-2000
C:Accession: J004863
R:Barthelemy, I.; Carramolino, L.; Gutterer, J.; Barbero, J.L.; Marquez, G.; Zaballós, Biochem. Biophys. Res. Commun. 224, 870-876, 1996
A>Title: zhx-1: A novel mouse homeodomain protein containing two zinc-fingers and five H
A:Reference number: JC4863; MID:96311380
A:Contents: bone
A:Accession: J004863
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-873 <BAR>
A:Cross-references: EMBL:254200; NID:92687851; PIDN:CAA90905.1; PID:91504088
C:Comment: This protein belongs to zinc-finger class of homeodomain transcription factor
C:Superfamily: unassigned homeobox proteins; homeobox homology
C:Keywords: bone; DNA binding; homeobox; nucleus; transcription regulation; zinc finger
F:70-93/Region: zinc finger
F:102-125/Region: zinc finger
F:285-341/Domain: homeobox homology <HOX1>
F:465-521/Domain: homeobox homology <HOX2>
F:569-625/Domain: homeobox homology <HOX3>
F:661-717/Domain: homeobox homology <HOX4>
F:741-765/Region: arginine/lysine-rich
F:771-827/Domain: homeobox homology <HOX5>

Query Match 53.1%; Score 51; DB 2; Length 873;
Best Local Similarity 61.1%; Pred. No. 9.1;

Matches 11; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 DSEDEEHITITDTELP 18
DB 844 DQDEDEETDSDTWERP 861

RESULT 6

JC7079
homeobox protein ZHX1 - human
C:Species: Homo sapiens (man)
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
C:Accession: J07079
R:Yamada, K.; Printz, R.L.; Osawa, H.; Graner, D.R.
Biochem. Biophys. Res. Commun. 261, 614-621, 1999
A>Title: Human ZHX1: Cloning, chromosomal location, and interaction with transcription
A:Reference number: J07079; MID:99373128
A:Accession: J07079
A:Molecule type: mRNA
A:Residues: 1-873 <YAM>
A:Cross-references: GB:AF106862; NID:95757883; PIDN:AMD50624.1; PID:95757884
A:Experimental source: liver
A:Genetics:
A:Gene: ZHX1
A:Map position: 8q
C:Superfamily: unassigned homeobox proteins; homeobox homology
C:Keywords: bone; DNA binding; homeobox; nucleus; transcription regulation; zinc finger
F:70-93/Region: zinc finger
F:102-125/Region: zinc finger
F:285-341/Domain: homeobox homology <HOX1>
F:465-521/Domain: homeobox homology <HOX2>
F:569-625/Domain: homeobox homology <HOX3>
F:661-717/Domain: homeobox homology <HOX4>

F:741-765/Region: arginine/lysine-rich
F:771-827/Domain: homeobox homology <HOX5>

Query Match 53.1%; Score 51; DB 2; Length 873;
Best Local Similarity 61.1%; Pred. No. 9.1;
Matches 11; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 DSEDEEHITITDTELP 18
DB 844 DQDEDEETDSDTWERP 861

RESULT 7

J0209
brain-specific angiogenesis inhibitor-associated protein 1 - human
N:Alternate names: BAI1-associated protein 1; BAP1 (tmsnmer)
C:Species: Homo sapiens (man)
C>Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 18-Aug-2000
C:Accession: J0209
R:Shtratsuch, T.; Putamura, M.; Oda, K.; Nishimori, H.; Nakamura, Y.; Tokino, T.
Biochem. Biophys. Res. Commun. 247, 597-604, 1998
A>Title: Cloning and characterization of BAI-associated protein 1: A PDZ domain-conta
A:Reference number: J0209; MID:98321173
A:Accession: J0209
A:Molecule type: mRNA
A:Residues: 1-1256 <SHI>
A:Cross-references: GB:AB010894; NID:93370997
A:Experimental source: brain
A:Genetics:
A:Gene: GDB:BAIAP1; BAP1
A:Cross-references: GDB:9864783
A:Map position: 3p14.1-3p14.1
C:Superfamily: WW repeat homology
F:300-337/Domain: WW repeat homology <WW1>
F:359-396/Domain: WW repeat homology <WW2>

Query Match 52.6%; Score 50.5; DB 2; Length 1256;
Best Local Similarity 61.1%; Pred. No. 17;

Matches 11; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

QY 1 DSEDEEHITITDTELP 18
DB 254 DSGQDEHT-LQETALPP 270

RESULT 8

A40437
glutamic acid-rich protein, retinal - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 05-Nov-1999
C:Accession: A40437
R:Sugimoto, Y.; Yatsunami, K.; Tsujimoto, M.; Khoreana, H.G.; Ichikawa, A.
Proc. Natl. Acad. Sci. U.S.A. 88, 3116-3119, 1991
A>Title: The amino acid sequence of a glutamic acid-rich protein from bovine retina
A:Reference number: A40437; MID:91195303
A:Accession: A40437
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-590 <SUG>
A:Cross-references: GB:M61185; NID:9163077; PIDN:AAA30536.1; PID:9163078

Query Match 51.0%; Score 49; DB 2; Length 590;
Best Local Similarity 38.9%; Pred. No. 12;
Matches 7; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 DSEDEEHITITDTELP 18
DB 459 DEEEDQHSVLDSTYLP 476

RESULT 9

S55352

IFH1 protein - yeast (Saccharomyces cerevisiae)

N:Alternate names: protein L8083.9; protein YLR223c; RRP3 protein

C:Species: Saccharomyces cerevisiae

C>Date: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jul-2000

C:Accession: S55352; S51446; S47477

R:Cherel, I.; Thuriaux, P.

Yeast 11, 261-270, 1995

A:Title: The IFH1 gene product interacts with a fork head protein in Saccharomyces cerevisiae

A:Reference number: S55352; MUID:95304839

A:Accession: S55352

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-285 <CHE>

A:Cross-references: EMBL:Z29488; NID:9531491; PIDN:CAA82624.1; PID:9531492

R:Hallsworth, K.

submitted to the EMBL Data Library, December 1994

A:Description: The sequence of S. cerevisiae cosmid 8083.

A:Reference number: S51443

A:Accession: S51446

A:Molecule type: DNA

A:Residues: 1-1085 <HAL>

A:Cross-references: EMBL:U19027; NID:9609363; PID:9609372; MIPS:YLR223c

C:Genetics:

A:Gene: SGD:IFH1; RRP3

A:Cross-references: SGD:S0004213; MIPS:YLR223c

A:Map position: 12R

Query Match 50.0%; Score 48; DB 2; Length 1085;

Best Local Similarity 47.1%; Pred. No. 35;

Matches 8; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 DSEDEEHTITDTELP 17

DB 404 DEEDDEEIMSDMP 420

RESULT 10

A49457

fibulin-2 precursor - mouse

C:Species: Mus musculus (house mouse)

C>Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 11-Jan-2000

C:Accession: A49457; S74095

R:Pan, T.C.; Sasaki, T.; Zhang, R.Z.; Faessler, R.; Timpl, R.; Chu, M.L.

J. Cell Biol. 123, 1269-1277, 1993

A:Title: Structure and expression of fibulin-2, a novel extracellular matrix protein with

A:Reference number: A49457; MUID:94064787

A:Accession: A49457

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1221 <PAN>

A:Cross-references: GB:X75285; NID:9437046; PIDN:CAA53040.1; PID:9437047

R:Sasaki, T.; Mann, K.; Murphy, G.; Chu, M.L.; Timpl, R.

Eur. J. Biochem. 240, 427-434, 1996

A:Title: Different susceptibilities of fibulin-1 and fibulin-2 to cleavage by matrix met

A:Reference number: S74094; MUID:96439073

A:Accession: S74095

A:Molecule type: protein

A:Residues: 236-238, 'X', 240-247; 260-275; 336-344, 'L', 346-361; 405-426; 566-568, 'EM', 569-589

A:Superfamily: unassigned EGF-related proteins; EGF homology

C:Keywords: calcium binding; duplication; extracellular matrix; glycoprotein; homotrimer

F:942-978/Domain: EGF homology <EGF>

Query Match 49.5%; Score 47.5; DB 2; Length 1221;

Best Local Similarity 50.0%; Pred. No. 48;

Matches 9; Conservative 4; Mismatches 2; Indels 3; Gaps 1;

QY 1 DSEDEEHTITDTELP 18

DB 274 DEEEETLTVTE---PP 288

RESULT 11

S12143

lipoprotein-associated coagulation inhibitor precursor - rabbit

N:Alternate names: endothelial cell coagulation inhibitor; endothelial cell tissue 2c

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Jul-1999

C:Accession: S12143; A61373

R:Wesselschmidt, R.L.; Girard, T.J.; Broze Jr., G.J.

Nucleic Acids Res. 18, 6440, 1990

A:Title: cDNA sequence of rabbit lipoprotein-associated coagulation inhibitor.

A:Reference number: S12143; MUID:91057146

A:Accession: S12143

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-300 <WES>

A:Cross-references: EMBL:X54708; NID:91612; PIDN:CAA38515.1; PID:91613

R:Colburn, P.; Crabb, J.W.; Buonassisi, V.

J. Cell. Physiol. 148, 320-326, 1991

A:Title: Enhanced inhibition of tissue factor by the extended form of an endothelial

A:Reference number: A61373; MUID:91349227

A:Accession: A61373

A:Molecule type: protein

A:Residues: 25-33, 'X', 35-46 <COL>

A:Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor

C:Keywords: anticoagulant; glycoprotein

F:50-100/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>

F:121-171/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>

F:213-263/Domain: animal Kunitz-type proteinase inhibitor homology <BP3>

Query Match 49.0%; Score 47; DB 2; Length 300;

Best Local Similarity 62.5%; Pred. No. 11;

Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 SEDEEHTITDTELP 17

DB 26 AEDEEFTNITDKPP 41

RESULT 12

S69063

probable membrane protein YPR075c - yeast (Saccharomyces cerevisiae)

N:Alternate names: hypothetical protein P9513.9

C:Species: Saccharomyces cerevisiae

C>Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 06-Feb-1998

C:Accession: S69063

R:Couch, J.

submitted to the EMBL Data Library, March 1996

A:Description: The sequence of S. cerevisiae cosmid 9513.

A:Reference number: S69057

A:Accession: S69063

A:Molecule type: DNA

A:Residues: 1-360 <COU>

A:Cross-references: EMBL:U51033; NID:91230676; PID:91230683; MIPS:YPR075c

C:Genetics:

A:Gene: SGD:OPY2

A:Cross-references: SGD:S0006279; MIPS:YPR075c

A:Map position: 16R

C:Keywords: transmembrane protein

F:96-112/Domain: transmembrane #status predicted <TM>

Query Match 49.0%; Score 47; DB 2; Length 360;

Best Local Similarity 47.1%; Pred. No. 13;

Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 DSEDEEHTITDTELP 17

DB 318 DEEDDEEGSFILDEIP 334

RESULT 13
 A:Accession: M1209
 A:Species: *Escherichia coli* (strain 8739) (NC_003110)
 C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 31-Dec-2001
 C:Accession: M1209
 R:Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, J.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entlian, K.D.; Fsihl, H.; Jones, L.M.; Karst, U.
 Science 294, 849-852, 2001
 A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurepka, G.; Madeno, E.; Maltournam, A.; Meok, C.; Schuierer, T.; Simoes, N.; Trierer, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of *Escherichia coli* strains
 A:Reference number: AB1077; PMID:21537279; PMID:11679669
 A:Accession: M1209
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-572 <GLA>
 A:Cross-References: GB:NC_003110; PIDN:GAC99154.1; PID:g16410478; GSPDB:GN00177
 A:Experimental source: strain EGD-e
 C:Genetics:
 A:Gene: lmo1076
 C:Keywords: hydrolase

Query Match 47.9%; Score 46; DB 2; Length 572;
 Best Local Similarity 44.4%; Pred. No. 33;
 Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 1 DSEDEEHHTITDTELP 18
 DB 34 DSEGEEDNFEVAREMPP 51

RESULT 14
 A:Accession: A46719
 A:Species: *Rattus norvegicus* (Norway rat)
 C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 20-Aug-1999
 C:Accession: A46719
 R:Blondel, O.; Takeda, J.; Janssen, H.; Selno, S.; Bell, G.I.
 J. Biol. Chem. 268, 11356-11363, 1993
 A:Title: Sequence and functional characterization of a third inositol trisphosphate receptor
 A:Reference number: A46719; PMID:9326594
 A:Accession: A46719
 A:Status: preliminary
 A:Molecule type: nucleic acid
 A:Residues: 1-2670 <BLD>
 A:Cross-References: GB:I06096; NID:g310170; PIDN:AAA41446.1; PID:g310171
 A:Experimental source: insulinoma cell line RINm5F
 A:Note: sequence extracted from NCBI database (NCBI:132840, NCBI:132841)
 C:Superfamily: inositol-trisphosphate receptor

Query Match 47.9%; Score 46; DB 2; Length 2670;
 Best Local Similarity 53.8%; Pred. No. 2.1e+02;
 Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 4 EDEHHTITDTELP 16
 DB 957 EDNEHTVVMETKL 969

RESULT 15
 A:Accession: T20784
 A:Species: *Caenorhabditis elegans*
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T20784
 R:Mortimore, B.; Basham, V.
 submitted to the EMBL Data Library, November 1996
 A:Reference number: Z19323
 A:Accession: T20784

A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-244 <MIL>
 A:Cross-References: EMBL:Z81500; PIDN:CA04102.1; GSPDB:GN00023; CESP:FL1D11.7
 A:Experimental source: clone FL1D11
 C:Genetics:
 A:Gene: CESP:FL1D11.7
 A:Map position: 5
 A:introns: 90/3; 185/1; 212/3

Query Match 46.9%; Score 45; DB 2; Length 244;
 Best Local Similarity 47.1%; Pred. No. 17;
 Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 1 DSEDEEHHTITDTELP 17
 DB 78 ESDRSEEHYVAIKTELP 94

Search completed: September 20, 2002, 10:28:02
 Job time: 45 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 20, 2002, 10:27:17 : Search time 105.99 Seconds
(without alignments)
59.776 Million cell updates/sec

Title: US-08-854-764-7

Perfect score: 96
Sequence: 1 DSEDEEHITITDELPP 18

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Pending_Patents_AA_Main:*

1: /cgn2_6/ptodata/2/paa/PCRUS_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/US06_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US07_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US08_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/US081_COMB.pep:*
6: /cgn2_6/ptodata/2/paa/US082_COMB.pep:*
7: /cgn2_6/ptodata/2/paa/US083_COMB.pep:*
8: /cgn2_6/ptodata/2/paa/US084_COMB.pep:*
9: /cgn2_6/ptodata/2/paa/US085_COMB.pep:*
10: /cgn2_6/ptodata/2/paa/US086_COMB.pep:*
11: /cgn2_6/ptodata/2/paa/US087_COMB.pep:*
12: /cgn2_6/ptodata/2/paa/US088_COMB.pep:*
13: /cgn2_6/ptodata/2/paa/US089_COMB.pep:*
14: /cgn2_6/ptodata/2/paa/US090_COMB.pep:*
15: /cgn2_6/ptodata/2/paa/US091_COMB.pep:*
16: /cgn2_6/ptodata/2/paa/US092_COMB.pep:*
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22: /cgn2_6/ptodata/2/paa/US098_COMB.pep:*
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25: /cgn2_6/ptodata/2/paa/US101_COMB.pep:*
26: /cgn2_6/ptodata/2/paa/US60_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	96	100.0	18	6	US-08-286-530-7
2	96	100.0	66	22	US-09-834-366-13745
3	96	100.0	66	22	US-09-834-366-18388
4	96	100.0	66	26	US-60-197-873-13745
5	96	100.0	66	26	US-60-197-873-18388
6	96	100.0	79	22	US-09-834-366-13738
7	96	100.0	79	26	US-60-197-873-13738

8	96	100.0	132	6	US-08-276-224-10	Sequence 10, App1
9	96	100.0 <td>132</td> <td>6</td> <td>US-08-279-753-10<td>Sequence 10, App1</td></td>	132	6	US-08-279-753-10 <td>Sequence 10, App1</td>	Sequence 10, App1
10	96	100.0 <td>132</td> <td>6</td> <td>US-08-279-753-10<td>Sequence 10, App1</td></td>	132	6	US-08-279-753-10 <td>Sequence 10, App1</td>	Sequence 10, App1
11	96	100.0 <td>152</td> <td>23</td> <td>US-09-924-340-94<td>Sequence 94, App1</td></td>	152	23	US-09-924-340-94 <td>Sequence 94, App1</td>	Sequence 94, App1
12	96	100.0 <td>152</td> <td>23</td> <td>US-09-994-590-94<td>Sequence 94, App1</td></td>	152	23	US-09-994-590-94 <td>Sequence 94, App1</td>	Sequence 94, App1
13	96	100.0 <td>152</td> <td>24</td> <td>US-10-000-489-94<td>Sequence 94, App1</td></td>	152	24	US-10-000-489-94 <td>Sequence 94, App1</td>	Sequence 94, App1
14	96	100.0 <td>152</td> <td>24</td> <td>US-10-000-986-94<td>Sequence 94, App1</td></td>	152	24	US-10-000-986-94 <td>Sequence 94, App1</td>	Sequence 94, App1
15	96	100.0 <td>151</td> <td>21</td> <td>US-09-741-106-19<td>Sequence 19, App1</td></td>	151	21	US-09-741-106-19 <td>Sequence 19, App1</td>	Sequence 19, App1
16	96	100.0 <td>164</td> <td>23</td> <td>US-09-924-340-96<td>Sequence 96, App1</td></td>	164	23	US-09-924-340-96 <td>Sequence 96, App1</td>	Sequence 96, App1
17	96	100.0 <td>164</td> <td>23</td> <td>US-09-994-590-96<td>Sequence 96, App1</td></td>	164	23	US-09-994-590-96 <td>Sequence 96, App1</td>	Sequence 96, App1
18	96	100.0 <td>164</td> <td>24</td> <td>US-10-000-489-96<td>Sequence 96, App1</td></td>	164	24	US-10-000-489-96 <td>Sequence 96, App1</td>	Sequence 96, App1
19	96	100.0 <td>164</td> <td>24</td> <td>US-10-000-986-96<td>Sequence 96, App1</td></td>	164	24	US-10-000-986-96 <td>Sequence 96, App1</td>	Sequence 96, App1
20	96	100.0 <td>164</td> <td>26</td> <td>US-60-305-456-96<td>Sequence 96, App1</td></td>	164	26	US-60-305-456-96 <td>Sequence 96, App1</td>	Sequence 96, App1
21	96	100.0 <td>210</td> <td>4</td> <td>US-08-026-146-8<td>Sequence 8, App1</td></td>	210	4	US-08-026-146-8 <td>Sequence 8, App1</td>	Sequence 8, App1
22	96	100.0 <td>276</td> <td>4</td> <td>US-08-085-126-116<td>Sequence 116, App</td></td>	276	4	US-08-085-126-116 <td>Sequence 116, App</td>	Sequence 116, App
23	96	100.0 <td>276</td> <td>6</td> <td>US-08-286-530-3<td>Sequence 3, App1</td></td>	276	6	US-08-286-530-3 <td>Sequence 3, App1</td>	Sequence 3, App1
24	96	100.0 <td>276</td> <td>8</td> <td>US-08-438-114-116<td>Sequence 116, App</td></td>	276	8	US-08-438-114-116 <td>Sequence 116, App</td>	Sequence 116, App
25	96	100.0 <td>276</td> <td>15</td> <td>US-09-130-273-1<td>Sequence 1, App1</td></td>	276	15	US-09-130-273-1 <td>Sequence 1, App1</td>	Sequence 1, App1
26	96	100.0 <td>276</td> <td>15</td> <td>US-09-227-955-1<td>Sequence 1, App1</td></td>	276	15	US-09-227-955-1 <td>Sequence 1, App1</td>	Sequence 1, App1
27	96	100.0 <td>276</td> <td>16</td> <td>US-09-265-468-1<td>Sequence 1, App1</td></td>	276	16	US-09-265-468-1 <td>Sequence 1, App1</td>	Sequence 1, App1
28	96	100.0 <td>276</td> <td>21</td> <td>US-09-741-106-9<td>Sequence 9, App1</td></td>	276	21	US-09-741-106-9 <td>Sequence 9, App1</td>	Sequence 9, App1
29	96	100.0 <td>276</td> <td>21</td> <td>US-09-766-778-1<td>Sequence 1, App1</td></td>	276	21	US-09-766-778-1 <td>Sequence 1, App1</td>	Sequence 1, App1
30	96	100.0 <td>291</td> <td>23</td> <td>US-09-924-340-48<td>Sequence 48, App1</td></td>	291	23	US-09-924-340-48 <td>Sequence 48, App1</td>	Sequence 48, App1
31	96	100.0 <td>291</td> <td>23</td> <td>US-09-924-340-52<td>Sequence 52, App1</td></td>	291	23	US-09-924-340-52 <td>Sequence 52, App1</td>	Sequence 52, App1
32	96	100.0 <td>291</td> <td>23</td> <td>US-09-994-590-48<td>Sequence 48, App1</td></td>	291	23	US-09-994-590-48 <td>Sequence 48, App1</td>	Sequence 48, App1
33	96	100.0 <td>291</td> <td>23</td> <td>US-09-994-590-52<td>Sequence 52, App1</td></td>	291	23	US-09-994-590-52 <td>Sequence 52, App1</td>	Sequence 52, App1
34	96	100.0 <td>291</td> <td>24</td> <td>US-10-000-489-48<td>Sequence 48, App1</td></td>	291	24	US-10-000-489-48 <td>Sequence 48, App1</td>	Sequence 48, App1
35	96	100.0 <td>291</td> <td>24</td> <td>US-10-000-986-48<td>Sequence 48, App1</td></td>	291	24	US-10-000-986-48 <td>Sequence 48, App1</td>	Sequence 48, App1
36	96	100.0 <td>291</td> <td>24</td> <td>US-10-000-986-52<td>Sequence 52, App1</td></td>	291	24	US-10-000-986-52 <td>Sequence 52, App1</td>	Sequence 52, App1
37	96	100.0 <td>291</td> <td>24</td> <td>US-10-000-986-52<td>Sequence 52, App1</td></td>	291	24	US-10-000-986-52 <td>Sequence 52, App1</td>	Sequence 52, App1
38	96	100.0 <td>291</td> <td>26</td> <td>US-60-305-456-48<td>Sequence 48, App1</td></td>	291	26	US-60-305-456-48 <td>Sequence 48, App1</td>	Sequence 48, App1
39	96	100.0 <td>291</td> <td>26</td> <td>US-60-305-456-52<td>Sequence 52, App1</td></td>	291	26	US-60-305-456-52 <td>Sequence 52, App1</td>	Sequence 52, App1
40	96	100.0 <td>304</td> <td>4</td> <td>US-08-026-146-2<td>Sequence 2, App1</td></td>	304	4	US-08-026-146-2 <td>Sequence 2, App1</td>	Sequence 2, App1
41	96	100.0 <td>304</td> <td>5</td> <td>US-08-179-660-23<td>Sequence 23, App1</td></td>	304	5	US-08-179-660-23 <td>Sequence 23, App1</td>	Sequence 23, App1
42	96	100.0 <td>304</td> <td>6</td> <td>US-08-208-264-25<td>Sequence 25, App1</td></td>	304	6	US-08-208-264-25 <td>Sequence 25, App1</td>	Sequence 25, App1
43	96	100.0 <td>304</td> <td>14</td> <td>US-08-676-125-18<td>Sequence 18, App1</td></td>	304	14	US-08-676-125-18 <td>Sequence 18, App1</td>	Sequence 18, App1
44	96	100.0 <td>304</td> <td>14</td> <td>US-09-054-272-16<td>Sequence 16, App1</td></td>	304	14	US-09-054-272-16 <td>Sequence 16, App1</td>	Sequence 16, App1
45	96	100.0 <td>304</td> <td>15</td> <td>US-09-136-012-18<td>Sequence 18, App1</td></td>	304	15	US-09-136-012-18 <td>Sequence 18, App1</td>	Sequence 18, App1

ALIGNMENTS

RESULT 1

US-08-286-530-7

Sequence 7, Application US/08286530

GENERAL INFORMATION:

APPLICANT: Innes, Michael

INVENTOR: Creasey, Abha

TITLE OF INVENTION: Production of Tissue Factor Pathway

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: Chiron Corporation

STREET: 4560 Horton St.

CITY: Emeryville

STATE: CA

COUNTRY: USA

ZIP: 94608

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30B

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/286,530

FILING DATE: 05-AUG-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Seaveride, Paul B.

REGISTRATION NUMBER: 36,914

REFERENCE/DOCKET NUMBER: 0991.001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 510-601-2585
TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 718 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-286-530-7

Query Match 100.0%; Score 96; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSEDEEHTIITDTLPP 18
|||||
DB 1 DSEDEEHTIITDTLPP 18

RESULT 2

US-09-834-366-13745
; Sequence 13745, Application US/09834366
; GENERAL INFORMATION:
; APPLICANT: Bejanin, Stephane
; APPLICANT: Tanaka, Hiroaki
; APPLICANT: Dumas Milne Edwards, Jean Baptiste
; APPLICANT: Jobert, Severin
; APPLICANT: Giordano, Jean-Yves
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: 81.US2.REG
; CURRENT APPLICATION NUMBER: US/09/834,366
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/197,873
; PRIOR FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 52153
; SOFTWARE: Patent.pm
; SEQ ID NO 13745
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -28...-1
; NAME/KEY: UNSURE
; LOCATION: 30
; OTHER INFORMATION: Xaa - Ala, Gly
US-09-834-366-13745

Query Match 100.0%; Score 96; DB 22; Length 66;
Best Local Similarity 100.0%; Pred. No. 2.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSEDEEHTIITDTLPP 18
|||||
DB 29 DSEDEEHTIITDTLPP 46

RESULT 3

US-09-834-366-18388
; Sequence 18388, Application US/09834366
; GENERAL INFORMATION:
; APPLICANT: Bejanin, Stephane
; APPLICANT: Tanaka, Hiroaki
; APPLICANT: Dumas Milne Edwards, Jean Baptiste
; APPLICANT: Jobert, Severin
; APPLICANT: Giordano, Jean-Yves
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: 81.US2.REG
; CURRENT APPLICATION NUMBER: US/09/834,366
; CURRENT FILING DATE: 2001-04-13

; PRIOR APPLICATION NUMBER: US 60/197,873
; PRIOR FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 52153
; SOFTWARE: Patent.pm
; SEQ ID NO 18388
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -28...-1
US-09-834-366-18388

Query Match 100.0%; Score 96; DB 22; Length 66;
Best Local Similarity 100.0%; Pred. No. 2.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSEDEEHTIITDTLPP 18
|||||
DB 29 DSEDEEHTIITDTLPP 46

RESULT 4

US-60-197-873-13745
; Sequence 13745, Application US/60197873
; GENERAL INFORMATION:
; APPLICANT: Bejanin, Stephane
; APPLICANT: Tanaka, Hiroaki
; APPLICANT: Dumas Milne Edwards, Jean Baptiste
; APPLICANT: Jobert, Severin
; APPLICANT: Giordano, Jean-Yves
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: 81.US1.PRO
; CURRENT APPLICATION NUMBER: US/60/197,873
; CURRENT FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 52153
; SOFTWARE: Patent.pm
; SEQ ID NO 13745
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -28...-1
; NAME/KEY: UNSURE
; LOCATION: 30
; OTHER INFORMATION: Xaa - Ala, Gly
US-60-197-873-13745

Query Match 100.0%; Score 96; DB 26; Length 66;
Best Local Similarity 100.0%; Pred. No. 2.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSEDEEHTIITDTLPP 18
|||||
DB 29 DSEDEEHTIITDTLPP 46

RESULT 5

US-60-197-873-18388
; Sequence 18388, Application US/60197873
; GENERAL INFORMATION:
; APPLICANT: Bejanin, Stephane
; APPLICANT: Tanaka, Hiroaki
; APPLICANT: Dumas Milne Edwards, Jean Baptiste
; APPLICANT: Jobert, Severin
; APPLICANT: Giordano, Jean-Yves
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: 81.US1.PRO
; CURRENT APPLICATION NUMBER: US/60/197,873
; CURRENT FILING DATE: 2000-04-18

NUMBER OF SEQ ID NOS: 52153
SOFTWARE: Patent.pm
SEQ ID NO 18388
LENGTH: 66
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: -28...-1
US-60-197-873-18388

Query Match 100.0%; Score 96; DB 26; Length 66;
Best Local Similarity 100.0%; Pred. No. 2.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSEDEHHTITDTLPP 18
|||||
Db 29 DSEDEHHTITDTLPP 46

RESULT 6
US-09-834-366-13738
Sequence 13738, Application US/09834366
GENERAL INFORMATION:
APPLICANT: Bejani, Stephane
APPLICANT: Tanaka, Hiroaki
APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Jobert, Severin
APPLICANT: Giordano, Jean-Yves
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: 81, US2, REG
CURRENT APPLICATION NUMBER: US/09/834,366
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: US 60/197,873
PRIOR FILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 52153
SOFTWARE: Patent.pm
SEQ ID NO 13738
LENGTH: 79
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: -28...-1
US-09-834-366-13738

Query Match 100.0%; Score 96; DB 22; Length 79;
Best Local Similarity 100.0%; Pred. No. 3.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSEDEHHTITDTLPP 18
|||||
Db 29 DSEDEHHTITDTLPP 46

RESULT 7
US-60-197-873-13738
Sequence 13738, Application US/60197873
GENERAL INFORMATION:
APPLICANT: Bejani, Stephane
APPLICANT: Tanaka, Hiroaki
APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Jobert, Severin
APPLICANT: Giordano, Jean-Yves
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: 81, US1, PRO
CURRENT APPLICATION NUMBER: US/60/197,873
CURRENT FILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 52153
SOFTWARE: Patent.pm
SEQ ID NO 13738

LENGTH: 79
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: -28...-1
US-60-197-873-13738

Query Match 100.0%; Score 96; DB 26; Length 79;
Best Local Similarity 100.0%; Pred. No. 3.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSEDEHHTITDTLPP 18
|||||
Db 29 DSEDEHHTITDTLPP 46

RESULT 8
US-08-276-224-10
Sequence 10, Application US/08276224
GENERAL INFORMATION:
APPLICANT: Norris, Fanny
APPLICANT: Norris, Kjeld
APPLICANT: Bjorn, Soren Erik
APPLICANT: Petersen, Lars Christian
APPLICANT: Olsen, Ole Hvilsted
TITLE OF INVENTION: A Human Kunitz-Type Protease Inhibitor
TITLE OF INVENTION: Variant
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Novo Nordisk of North America, Inc.
STREET: 405 Lexington Avenue, Suite 6400
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,224
FILING DATE: 15-JUL-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK92/00002
FILING DATE: 07-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK92/00340
FILING DATE: 16-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK93/00005
FILING DATE: 07-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/021,605
FILING DATE: 22-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Lowmey, Karen A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 3692.210-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-276-224-10

Query Match 100.0%; Score 96; DB 6; Length 132;
Best Local Similarity 100.0%; Pred. No. 6e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSEDEEHTIITDTELP 18
Db 54 DSEDEEHTIITDTELP 71

RESULT 9

US-08-279-753-10
Sequence 10, Application US/08279753
GENERAL INFORMATION:
APPLICANT: Norris, Fanny
TITLE OF INVENTION: A Human Kunitz-Type Protease Inhibitor
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Novo Nordisk of North America, Inc.
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/279,753
FILING DATE: 21-JUL-1994
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK92/00002
FILING DATE: 07-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK92/00340
FILING DATE: 16-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/021,605
FILING DATE: 22-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Lowney, Karen A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 3692.220-US
TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-279-753-10

Query Match 100.0%; Score 96; DB 6; Length 132;
Best Local Similarity 100.0%; Pred. No. 6e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSEDEEHTIITDTELP 18
Db 54 DSEDEEHTIITDTELP 71

RESULT 10

US-08-279-753A-10

Sequence 10, Application US/08279753A
GENERAL INFORMATION:
APPLICANT: Norris, Fanny
TITLE OF INVENTION: A Human Kunitz-Type Protease Inhibitor
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Novo Nordisk of North America, Inc.
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/279,753A
FILING DATE: 21-JUL-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK92/00002
FILING DATE: 07-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK92/00340
FILING DATE: 16-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK93/00005
FILING DATE: 07-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/021,605
FILING DATE: 22-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Gregg, Valeta A.
REGISTRATION NUMBER: 35,127
REFERENCE/DOCKET NUMBER: 3692.220-US
TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-279-753A-10

Query Match 100.0%; Score 96; DB 6; Length 132;
Best Local Similarity 100.0%; Pred. No. 6e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSEDEEHTIITDTELP 18
Db 54 DSEDEEHTIITDTELP 71

RESULT 11

US-09-924-340-94
Sequence 94, Application US/09924340
GENERAL INFORMATION:
APPLICANT: Bejanin, Stephane
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF.
FILE REFERENCE: 91.US2.REG
CURRENT APPLICATION NUMBER: US/09/924,340
CURRENT FILING DATE: 2001-08-06

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;; PRIOR APPLICATION NUMBER: US 60/305,456
;; PRIOR FILING DATE: 2001-07-13
;; PRIOR APPLICATION NUMBER: US 60/302,277
;; PRIOR FILING DATE: 2001-06-29
;; PRIOR APPLICATION NUMBER: US 60/298,698
;; PRIOR FILING DATE: 2001-06-15
;; PRIOR APPLICATION NUMBER: US 60/293,574
;; PRIOR FILING DATE: 2001-05-25
;; NUMBER OF SEQ ID NOS: 112
;; SOFTWARE: Jpatent
;; SEQ ID NO 94
;; LENGTH: 152
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: SIGNAL
;; LOCATION: 1..19
US-09-924-340-94
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Query Match 100.0%; Score 96; DB 23; Length 152;
Best Local Similarity 100.0%; Pred. No. 7.2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1 DSEDEDEHTITDTELP 18
DB 20 DSEDEDEHTITDTELP 37
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```
RESULT 12
US-09-994-590-94
;; Sequence 94, Application US/09994590
;; GENERAL INFORMATION:
;; APPLICANT: Benjamin, Stephane
;; APPLICANT: Tanaka, Hiroaki
;; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
;; FILE REFERENCE: 91.US3.DIV
;; CURRENT APPLICATION NUMBER: US/09/994,590
;; PRIOR FILING DATE: 2001-11-13
;; PRIOR APPLICATION NUMBER: US 09/924,340
;; PRIOR FILING DATE: 2001-08-06
;; PRIOR APPLICATION NUMBER: PCT/IB01/01715
;; PRIOR FILING DATE: 2001-08-06
;; PRIOR APPLICATION NUMBER: US 60/305,456
;; PRIOR FILING DATE: 2001-07-13
;; PRIOR APPLICATION NUMBER: US 60/302,277
;; PRIOR FILING DATE: 2001-06-29
;; PRIOR APPLICATION NUMBER: US 60/298,698
;; PRIOR FILING DATE: 2001-06-15
;; PRIOR APPLICATION NUMBER: US 60/293,574
;; PRIOR FILING DATE: 2001-05-25
;; NUMBER OF SEQ ID NOS: 112
;; SOFTWARE: Jpatent
;; SEQ ID NO 94
;; LENGTH: 152
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: SIGNAL
;; LOCATION: 1..19
US-09-994-590-94
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Query Match 100.0%; Score 96; DB 23; Length 152;
Best Local Similarity 100.0%; Pred. No. 7.2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1 DSEDEDEHTITDTELP 18
DB 20 DSEDEDEHTITDTELP 37
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RESULT 13

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US-10-000-489-94
;; Sequence 94, Application US/10000489
;; GENERAL INFORMATION:
;; APPLICANT: Benjamin, Stephane
;; APPLICANT: Tanaka, Hiroaki
;; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
;; FILE REFERENCE: 91.US6.DIV
;; CURRENT APPLICATION NUMBER: US/10/000,489
;; PRIOR FILING DATE: 2001-11-14
;; PRIOR APPLICATION NUMBER: US 09/924,340
;; PRIOR FILING DATE: 2001-08-06
;; PRIOR APPLICATION NUMBER: PCT/IB01/01715
;; PRIOR FILING DATE: 2001-08-06
;; PRIOR APPLICATION NUMBER: US 60/305,456
;; PRIOR FILING DATE: 2001-07-13
;; PRIOR APPLICATION NUMBER: US 60/302,277
;; PRIOR FILING DATE: 2001-06-29
;; PRIOR APPLICATION NUMBER: US 60/298,698
;; PRIOR FILING DATE: 2001-06-15
;; PRIOR APPLICATION NUMBER: US 60/293,574
;; PRIOR FILING DATE: 2001-05-25
;; NUMBER OF SEQ ID NOS: 112
;; SOFTWARE: Jpatent
;; SEQ ID NO 94
;; LENGTH: 152
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: SIGNAL
;; LOCATION: 1..19
US-10-000-489-94
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Query Match 100.0%; Score 96; DB 24; Length 152;
Best Local Similarity 100.0%; Pred. No. 7.2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1 DSEDEDEHTITDTELP 18
DB 20 DSEDEDEHTITDTELP 37
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RESULT 14
US-10-000-986-94
;; Sequence 94, Application US/10000986
;; GENERAL INFORMATION:
;; APPLICANT: Benjamin, Stephane
;; APPLICANT: Tanaka, Hiroaki
;; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
;; FILE REFERENCE: 91.US9.DIV
;; CURRENT APPLICATION NUMBER: US/10/000,986
;; PRIOR FILING DATE: 2001-11-14
;; PRIOR APPLICATION NUMBER: US 09/924,340
;; PRIOR FILING DATE: 2001-08-06
;; PRIOR APPLICATION NUMBER: PCT/IB01/01715
;; PRIOR FILING DATE: 2001-08-06
;; PRIOR APPLICATION NUMBER: US 60/305,456
;; PRIOR FILING DATE: 2001-07-13
;; PRIOR APPLICATION NUMBER: US 60/302,277
;; PRIOR FILING DATE: 2001-06-29
;; PRIOR APPLICATION NUMBER: US 60/298,698
;; PRIOR FILING DATE: 2001-06-15
;; PRIOR APPLICATION NUMBER: US 60/293,574
;; PRIOR FILING DATE: 2001-05-25
;; NUMBER OF SEQ ID NOS: 112
;; SOFTWARE: Jpatent
;; SEQ ID NO 94
;; LENGTH: 152
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: SIGNAL
;; LOCATION: 1..19
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Fri Sep 20 10:48:18 2002

US-10-000-986-94

Query Match 100.0%; Score 96; DB 24; Length 152;
Best Local Similarity 100.0%; Pred. No. 7.2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DSEDEEHTITDTELP 18
Db 20 DSEDEEHTITDTELP 37

RESULT 15

US-09-741-106-19

; Sequence 19 Application US/097411106

GENERAL INFORMATION:

; APPLICANT: Innis, Michael

; Creasey, Abia

; TITLE OF INVENTION: Chimeric Proteins

; NUMBER OF SEQUENCES: 37

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Chiron Corporation

; STREET: 4560 Horton St.

; CITY: Emeryville

; STATE: CA

; COUNTRY: USA

; ZIP: 94608

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30B

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/741,106

; FILING DATE: 12-Dec-2000

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/286,521

; FILING DATE: 1994-08-05

; ATTORNEY/AGENT INFORMATION:

; NAME: Saveriede, Paul B.

; REGISTRATION NUMBER: 36,914

; REFERENCE/DOCKET NUMBER: 0990.001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 510-601-2585

; TELEFAX: 510-655-3542

; INFORMATION FOR SEQ ID NO: 19:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 161 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 19:

US-09-741-106-19

Query Match 100.0%; Score 96; DB 21; Length 161;
Best Local Similarity 100.0%; Pred. No. 7.8e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DSEDEEHTITDTELP 18
Db 1 DSEDEEHTITDTELP 18

Search completed: September 20, 2002, 10:30:30
Job time: 193 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 20, 2002, 10:27:42 : Search time 35.94 seconds
(without alignments)
133.977 Million cell updates/sec

Title: US-08-854-764-7

Perfect score: 96

Sequence: 1 DSEDEHITITDPELP 18

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 947138 seqs, 267508082 residues

Total number of hits satisfying chosen parameters: 947138

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08

Listing first 45 summaries

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7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	96	100.0	152	5 US-09-992-600A-94	Sequence 94, Appl
2	96	100.0	164	5 US-09-992-600A-96	Sequence 96, Appl
3	96	100.0	251	5 US-09-791-537-120691	Sequence 120691,
4	96	100.0	276	6 US-10-086-176-5	Sequence 5, Appl
5	96	100.0	276	6 US-10-086-176A-5	Sequence 5, Appl
6	96	100.0	291	5 US-09-992-600A-48	Sequence 48, Appl
7	96	100.0	291	5 US-09-992-600A-52	Sequence 52, Appl
8	96	100.0	304	5 US-09-791-537-101054	Sequence 101054,
9	96	100.0	304	6 US-10-167-351-1	Sequence 1,
10	90	93.8	304	5 US-09-791-537-15150	Sequence 15150, A
11	78	81.2	91	6 US-10-206-272-546	Sequence 546, App
12	63	65.6	103	6 US-10-206-272-547	Sequence 547, App
13	55	57.3	434	6 US-10-179-131-7632	Sequence 7632, Ap
14	51	53.1	100	6 US-10-211-346-468	Sequence 468, App
15	51	53.1	873	5 US-09-791-537-39142	Sequence 39142, A
16	51	53.1	873	5 US-09-791-537-126426	Sequence 126426,
17	50.5	52.6	224	6 US-10-185-050-50	Sequence 50, Appl
18	50.5	52.6	677	5 US-09-791-537-142737	Sequence 142737,
19	50.5	52.6	1256	5 US-09-791-537-76349	Sequence 76349, A
20	50.5	52.6	1256	5 US-09-791-537-107368	Sequence 107368,
21	49.5	51.6	526	6 US-10-104-047-3582	Sequence 3582, Ap
22	49.5	51.6	732	6 US-10-104-047-3474	Sequence 3474, Ap
23	49.5	51.6	1036	5 US-09-914-464-205	Sequence 205, App
24	47	49.0	300	5 US-09-791-537-1623	Sequence 1623, Ap
25	47	49.0	300	5 US-09-791-537-108592	Sequence 108592,
26	47	49.0	1179	5 US-09-791-537-72053	Sequence 72053, A

ALIGNMENTS

27	47	49.0	1189	5 US-09-791-537-11292	Sequence 11292, A
28	47	49.0	1189	5 US-09-791-537-68627	Sequence 68627, A
29	46	47.9	48	6 US-10-008-524A-153	Sequence 153, App
30	46	47.9	767	6 US-10-179-131-8385	Sequence 8385, Ap
31	46	47.9	830	6 US-10-179-131-8354	Sequence 8354, Ap
32	45	46.9	134	6 US-10-155-881-22243	Sequence 22243, A
33	45	46.9	259	5 US-09-791-537-118383	Sequence 118383,
34	45	46.9	291	6 US-10-155-881-109939	Sequence 109939, A
35	45	46.9	386	5 US-09-791-537-131924	Sequence 131924,
36	45	46.9	570	6 US-10-067-741-7	Sequence 7, Appl
37	45	46.9	578	6 US-10-106-698-636	Sequence 4636, Ap
38	45	46.9	576	5 US-09-458-180-2	Sequence 2, Appl
39	44.5	46.4	200	7 US-60-360-039-15654	Sequence 15654, A
40	44.5	46.4	200	7 US-60-360-039-16039	Sequence 16039, A
41	44	45.8	326	6 US-10-212-778-761	Sequence 761, App
42	44	45.8	441	6 US-10-155-881-18133	Sequence 18133, A
43	44	45.8	441	6 US-10-155-881-21041	Sequence 21041, A
44	44	45.8	441	6 US-10-155-881-31345	Sequence 31345, A
45	44	45.8	502	5 US-09-791-537-6416	Sequence 6416, Ap

RESULT 1.
US-09-992-600A-94
Sequence 94, Application US/09992600A
GENERAL INFORMATION:
APPLICANT: Benjamin, Stephane
APPLICANT: Tanaka, Hiroaki
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91.054.DIV
CURRENT APPLICATION NUMBER: US/09/992,600A
PRIOR APPLICATION NUMBER: US 09/924,340
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: PCT/IB01/01715
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/302,277
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/298,698
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 60/293,574
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 114
SOFTWARE: Jpatent
SEQ ID NO 94
LENGTH: 152
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: 1..19
US-09-992-600A-94

Query Match 100.0%; Score 96; DB 5; Length 152;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSEDEHITITDPELP 18
DB 20 DSEDEHITITDPELP 37

RESULT 2
US-09-992-600A-96
Sequence 96, Application US/09992600A
GENERAL INFORMATION:
APPLICANT: Benjamin, Stephane
APPLICANT: Tanaka, Hiroaki

RESULT 4
US-10-086-176-5
; Sequence 5, Application US/10086176
; GENERAL INFORMATION:
; APPLICANT: Hembrough, Todd
; APPLICANT: Papathanassiou, Adonia E.

Query Match	100.0%	Score 96;	DB 6;	Length 276;
Best Local Similarity	100.0%	Pred. NO. 3.3e-06;		
Matches 18;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;

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QY 1 DSEDEEHTIITDTELPP 18
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Db 1 DSEDEEHTIITDTELPP 18
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RESULT 6
US-09-992-600A-48
; Sequence 48, Application US/09992600A
; GENERAL INFORMATION:
; APPLICANT: Benjamin, Stephane
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 91.054.DIV
; CURRENT FILING DATE: 2001-11-13
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 09/924,340
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: PCT/IB01/01715
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: JPatent
; SEQ ID NO 48
; LENGTH: 291
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: 1..28
US-09-992-600A-48

Query Match          100.0%; Score 96; DB 5; Length 291;
Best Local Similarity 100.0%; Pred. No. 3.5e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSEDEDEHTITDTLPP 18
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DB 29 DSEDEDEHTITDTLPP 46

RESULT 7
US-09-992-600A-52
; Sequence 52, Application US/09992600A
; GENERAL INFORMATION:
; APPLICANT: Benjamin, Stephane
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 91.054.DIV
; CURRENT FILING DATE: 2001-11-13
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 09/924,340
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: PCT/IB01/01715
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: JPatent
; SEQ ID NO 52
; LENGTH: 291
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
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; NAME/KEY: SIGNAL
; LOCATION: 1..28
US-09-992-600A-52

Query Match          100.0%; Score 96; DB 5; Length 291;
Best Local Similarity 100.0%; Pred. No. 3.5e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSEDEDEHTITDTLPP 18
|||||
DB 29 DSEDEDEHTITDTLPP 46

RESULT 8
US-09-791-537-101054
; Sequence 101054, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Blonomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; FILE REFERENCE: 261/210
; CURRENT FILING DATE: 2001-02-22
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 101054
; LENGTH: 304
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-101054

Query Match          100.0%; Score 96; DB 5; Length 304;
Best Local Similarity 100.0%; Pred. No. 3.7e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSEDEDEHTITDTLPP 18
|||||
DB 29 DSEDEDEHTITDTLPP 46

RESULT 9
US-10-167-351-1
; Sequence 1, Application US/10167351
; GENERAL INFORMATION:
; APPLICANT: DYAX CORP.
; APPLICANT: Markland, William
; APPLICANT: Ladner, Robert C.
; TITLE OF INVENTION: Inhibitors of Human Plasmin Derived From The Kunitz Domains
; FILE REFERENCE: DYX-007.2P US-4
; CURRENT FILING DATE: 2002-06-11
; PRIOR FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: 09/638,770
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: 09/414,878
; PRIOR FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: 09/240,136
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 08/676,124
; PRIOR FILING DATE: 1997-01-07
; PRIOR APPLICATION NUMBER: PCT/US95/00298
; PRIOR FILING DATE: 1995-01-11
; PRIOR APPLICATION NUMBER: 08/208,265
; PRIOR FILING DATE: 1994-03-10
; PRIOR APPLICATION NUMBER: 08/179,658
; PRIOR FILING DATE: 1994-01-11
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 304
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-167-351-1

Query Match      100.0%; Score 96; DB 6; Length 304;
Best Local Similarity 100.0%; Pred. No. 3.7e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSEDEHTIITDTELP 18
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DB 29 DSEDEHTIITDTELP 46

RESULT 10
US-09-791-537-15150
; Sequence 15150, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15150
; LENGTH: 304
; TYPE: PRT
; ORGANISM: Macaca mulatta
US-09-791-537-15150

Query Match      93.8%; Score 90; DB 5; Length 304;
Best Local Similarity 94.4%; Pred. No. 2.9e-05;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSEDEHTIITDTELP 18
   |||||
DB 29 DSEDEHTIITDTELP 46

RESULT 11
US-10-206-272-546
; Sequence 546, Application US/10206272
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PM027C1N
; CURRENT APPLICATION NUMBER: US/10/206,272
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: 09/758,445
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 816
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 546
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (44)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (62)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids

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US-10-206-272-547

Query Match 65.6%; Score 63; DB 6; Length 103;
Best Local Similarity 80.0%; Pred. No. 0.076;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 DSEDEEHITITDTE 15
DB 29 DSEDEEHITITDTE 43

RESULT 13
US-10-179-131-7632

; Sequence 7632, Application US/10179131
; GENERAL INFORMATION:
; APPLICANT: HARE, ROBERTA S.
; APPLICANT: SHAW, KAREN J.
; APPLICANT: SHIRER JR., GEORGE H.
; APPLICANT: KESSLER, MARCO
; APPLICANT: NOLLING, JORK
; APPLICANT: ZENG, QIANDONG
; APPLICANT: GREENE, JONATHAN R.
; TITLE OF INVENTION: CANDIDA ALBICANS NUCLEIC ACIDS AND POLYPEPTIDES,
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: 2976-4031
; CURRENT APPLICATION NUMBER: US/10/179,131
; CURRENT FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 10194
; SEQ ID NO 7632
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Candida albicans
US-10-179-131-7632

Query Match 57.3%; Score 55; DB 6; Length 434;
Best Local Similarity 55.6%; Pred. No. 6.3;
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 1 DSEDEEHITITDTELP 18
DB 401 DSEDEEHITITDTELP 418

RESULT 14
US-10-211-346-468

; Sequence 468, Application US/10211346
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PM008CIN
; CURRENT APPLICATION NUMBER: US/10/211,346
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: 09/758,469
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 782
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 468
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-211-346-468

Query Match 53.1%; Score 51; DB 6; Length 100;
Best Local Similarity 61.1%; Pred. No. 4.3;
Matches 11; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

OY 1 DSEDEEHITITDTELP 18
DB 71 DSEDEEHITITDTELP 88

RESULT 15
US-09-791-537-39142

; Sequence 39142, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Biocomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 39142
; LENGTH: 873
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-39142

Query Match 53.1%; Score 51; DB 5; Length 873;
Best Local Similarity 61.1%; Pred. No. 56;
Matches 11; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

OY 1 DSEDEEHITITDTELP 18
DB 844 DSEDEEHITITDTELP 861

Search completed: September 20, 2002, 10:31:44
Job time: 242 sec

Strausberg R.,
Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
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SEQUENCE OF 29-50.
RX MEDLINE-90036996; PubMed-2553722;
RA Novotny W.F., Girard T.J., Miletich J.P., Broze G.J. Jr.;
RT "Purification and characterization of the lipoprotein-associated
coagulation inhibitor from human plasma";
RL J. Biol. Chem. 264:18832-18837(1989).
RN [8]
RN INHIBITORY SITES.
RX MEDLINE-89181950; PubMed-2927510;
RA Girard T.J., Warren L.A., Novotny W.F., Likert K.M., Brown S.G.,
RA Miletich J.P., Broze G.J. Jr.;
RT "Functional significance of the Kunitz-type inhibitory domains of
lipoprotein-associated coagulation inhibitor";
RL Nature 338:518-520(1989).
RN [9]
RN CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE-96224851; PubMed-8639592;
RA Nakahara Y., Miyata T., Hamuro T., Funatsu A., Miyagi M.,
RA Tsunashima S., Kato H.;
RT "Amino acid sequence and carbohydrate structure of a recombinant
human tissue factor pathway inhibitor expressed in Chinese hamster
ovary cells: one N- and two O-linked carbohydrate chains are located
between Kunitz domains 2 and 3 and one N-linked carbohydrate chain is
in Kunitz domain 2";
RL Biochemistry 35:6450-6459(1996).
RN [10]
RN REVIEW.
RX MEDLINE-91104709; PubMed-2271516;
RA Broze G.J. Jr., Girard T.J., Novotny W.F.;
RT "Regulation of coagulation by a multivalent Kunitz-type inhibitor";
RL Biochemistry 29:7539-7546(1990).
RN [11]
RN STRUCTURE BY NMR OF 121-182.
RX MEDLINE-97342711; PubMed-9199408;
RA Burgerling M.J., Orbons L.P., van der Doelen A., Mulders J.,
RA Theunissen H.J., Grootenhuys P.D., Bode W., Huber R., Stubbs M.T.;
RT "The second Kunitz domain of human tissue factor pathway inhibitor:
cloning, structure determination and interaction with factor Xa";
RL J. Mol. Biol. 269:395-407(1997).
CC -1- FUNCTION: INHIBITS FACTOR X (X(A)) DIRECTLY AND, IN A XA-DEPENDENT
WAY, INHIBITS VII(A)/TISSUE FACTOR ACTIVITY, PRESUMABLY BY FORMING
A QUATERNARY X(A)/LACI/VII(A)/TF COMPLEX. IT POSSESSES AN
ANTITHROMBOTIC ACTION AND ALSO THE ABILITY TO ASSOCIATE WITH
LIPOPROTEINS IN PLASMA.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; alpha/TPPIalpha (shown here) and
beta/TPPIbeta; are produced by alternative splicing.
CC -1- TISSUE SPECIFICITY: MOSTLY IN ENDOTHELIAL CELLS.
CC -1- DOMAIN: THIS INHIBITOR CONTAINS THREE INHIBITORY DOMAINS.
CC -1- PTM: O-GLYCOSYLATED.
CC -1- SIMILARITY: CONTAINS 3 BPTI/KUNITZ INHIBITOR DOMAINS.
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or send an email to license@isb-sib.ch).

DR EMBL; J03225; AAA59526.1; -
DR EMBL; M58650; AAA59480.1; -
DR EMBL; M58644; AAA59480.1; JOINED.
DR EMBL; M58645; AAA59480.1; JOINED.
DR EMBL; M58646; AAA59480.1; JOINED.
DR EMBL; M58647; AAA59480.1; JOINED.
DR EMBL; M58648; AAA59480.1; JOINED.
DR EMBL; M58649; AAA59480.1; JOINED.
DR EMBL; M59499; AAA59526.1; -
DR EMBL; M59493; AAA59526.1; JOINED.

DR EMBL; M59494; AAA59526.1; JOINED.
DR EMBL; M59495; AAA59526.1; JOINED.
DR EMBL; M59496; AAA59526.1; JOINED.
DR EMBL; M59497; AAA59526.1; JOINED.
DR EMBL; M59498; AAA59526.1; JOINED.
DR EMBL; AF021834; AAD01700.1; -
DR EMBL; BC015514; AAH15514.1; -
DR PIR; A28650; TIHUGK.
DR PIR; A34315; A34315.
DR PIR; A60433; A60433.
DR PIR; S03903; S03903.
DR PDB; 1ADZ; 25-FEB-98.
DR PDB; 1TFX; 21-JAN-98.
DR GlycoSuiteDB; P10646; -
DR MIM; 152310; -
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI; 3.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00131; KU; 3.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 3.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 3.
KW Serine protease inhibitor; Glycoprotein; Repeat; Blood coagulation;
KW Signal; Alternative splicing; 3D-structure; Polymorphism.
FT SIGNAL 1 28 TISSUE FACTOR PATHWAY INHIBITOR.
FT CHAIN 29 304 BPTI/KUNITZ INHIBITOR 1
FT DOMAIN 54 104 (VII(A)/TISSUE FACTOR BINDING SITE).
FT DOMAIN 125 175 BPTI/KUNITZ INHIBITOR 2
FT DOMAIN 217 267 (FACTOR X(A) BINDING SITE).
FT DISULFID 54 104 BPTI/KUNITZ INHIBITOR 3.
FT DISULFID 63 87 BY SIMILARITY.
FT DISULFID 79 100 BY SIMILARITY.
FT ACT_SITE 64 65 REACTIVE BOND (BY SIMILARITY).
FT DISULFID 125 175 BY SIMILARITY.
FT DISULFID 134 158 BY SIMILARITY.
FT DISULFID 150 171 BY SIMILARITY.
FT ACT_SITE 135 136 REACTIVE BOND (BY SIMILARITY).
FT DISULFID 217 267 BY SIMILARITY.
FT DISULFID 226 250 BY SIMILARITY.
FT ACT_SITE 227 228 REACTIVE BOND (BY SIMILARITY).
FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .).
FT CARBOHYD 202 202 O-LINKED.
FT CARBOHYD 203 203 O-LINKED.
FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .).
FT VARSPLIC 210 251 EFHGSPCLPAGRLGCRANENREYNSVIGKRPFKVSGC
FT VARSPLIC 252 304 G -> VTKEGNDGKNAHIYQVFLNAFCIHASMFELGLD
FT VARSPLIC 292 292 SISCLC (IN ISOFORM BETA).
FT MUTAGEN 64 64 MISSING (IN ISOFORM BETA).
FT MUTAGEN 135 135 V -> M (IN DBSNP:5940).
FT MUTAGEN 227 227 /FTID-VAR_012004.
FT SEQUENCE 304 AA; 35015 MW; 5281E32B758B44FE CRC64;
K->I: ABOLISHES INHIBITION OF VII(A)/TF.
R->L: ABOLISHES INHIBITION OF X(A).
R->L: ABOLISHES INHIBITION OF VII(A)/TF.
Query Match 100.0%; Score 96; DB 1; Length 304;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DSEDEEHTIITDELPP 18
DB 29 DSEDEEHTIITDELPP 46
RESULT 2
ID TFPI_MACHU STANDARD; PRT; 304 AA.
AC Q28864;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Tissue factor pathway inhibitor precursor (TFPI) (Lipoprotein-
 DE associated coagulation inhibitor) (LACI) (extrinsic pathway inhibitor)
 DE (EPI).
 GN TFPI OR TFPI1.
 OS Macaca mulatta (Rhesus macaque).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 CC Cercopithecidae; Macaca.
 CC NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-FACTOR.
 RX MEDLINE-94375417; PubMed-8089087;
 RA Kamei S., Kamikado Y., Hamuro T., Fujimoto H., Ishihara M.,
 RA Ionomura H., Miyamoto S., Funatsu A., Enjoji K., Abumiya T.;
 RT Amino acid sequence and inhibitory activity of rhesus monkey tissue
 RT factor pathway inhibitor (TFPI): comparison with human TFPI*.
 RL J. Biochem. 115:708-714(1994).
 CC -1- FUNCTION: INHIBITS FACTOR X (X(A)) DIRECTLY AND, IN A XA-DEPENDENT
 CC WAY, INHIBITS VII(A)/TISSUE FACTOR ACTIVITY, PRESUMABLY BY FORMING
 CC A QUATERNARY X(A)/LACI/VII(A)/TF COMPLEX. IT POSSESSES AN
 CC ANTITHROMBOTIC ACTION AND ALSO THE ABILITY TO ASSOCIATE WITH
 CC LIPOPROTEINS IN PLASMA.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DOMAIN: THIS INHIBITOR CONTAINS THREE INHIBITORY DOMAINS.
 CC -1- PTM: O-GLYCOSYLATED (BY SIMILARITY).
 CC -1- SIMILARITY: CONTAINS 3 BPTI/KUNITZ INHIBITOR DOMAINS.
 CC -----
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 CC -----
 CC EMBL: S73337; AAB31955.1; -
 CC HSSP: P10646; ITEX.
 DR InterPro: IPR002223; Kunitz_BPTI.
 DR Pfam: PF00014; Kunitz_BPTI; 3.
 DR PRINTS: PR00759; BASICPTASE.
 DR SMART: SM00131; KU; 3.
 DR PROSITE: PS00280; BPTI_KUNITZ_1; 3.
 DR PROSITE: PS50279; BPTI_KUNITZ_2; 3.
 KM Serine protease inhibitor; Glycoprotein; Repeat; Blood coagulation;
 FT SIGNAL. 1 28 BY SIMILARITY.
 FT CHAIN 29 304 TISSUE FACTOR PATHWAY INHIBITOR.
 FT DOMAIN 54 104 BPTI/KUNITZ INHIBITOR 1
 FT (VII(A)/TISSUE FACTOR BINDING SITE).
 FT DOMAIN 125 175 BPTI/KUNITZ INHIBITOR 2
 FT (FACTOR X(A) BINDING SITE).
 FT DOMAIN 217 267 BPTI/KUNITZ INHIBITOR 3.
 FT DISULFID 54 104 BY SIMILARITY.
 FT DISULFID 63 107 BY SIMILARITY.
 FT DISULFID 79 100 BY SIMILARITY.
 FT ACT_SITE 64 65 REACTIVE BOND (BY SIMILARITY).
 FT DISULFID 125 175 BY SIMILARITY.
 FT ACT_SITE 134 158 BY SIMILARITY.
 FT DISULFID 150 171 BY SIMILARITY.
 FT ACT_SITE 135 136 REACTIVE BOND (BY SIMILARITY).
 FT DISULFID 217 267 BY SIMILARITY.
 FT DISULFID 226 250 BY SIMILARITY.
 FT DISULFID 242 263 BY SIMILARITY.
 FT ACT_SITE 227 228 REACTIVE BOND (BY SIMILARITY).
 FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 256 256 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 304 AA; 35085 MW; 56E13B3FF16282B0 CRC64;

Query Match

93.8%; Score 90; DB 1; Length 304;

Best Local Similarity 94.4%; Pred. No. 1, le-06;
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 DSEDEERTITDTLELP 18
 |||||:|||||||
 Db 29 DSEDEERTITDTLELP 46
 RESULT 3
 ID R115_YEAST STANDARD; PRT: 1770 AA.
 AC P43565;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Serine/threonine-protein kinase Rlm15 (EC 2.7.1.1.-).
 GN RIM15 OR TAK1 OR YFL033C.
 OS Saccharomyces cerevisiae (Baker's yeast).
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetaceae; Saccharomycetaceae; Saccharomycetes.
 CC NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-S288C / AB972;
 RX MEDLINE-95400292; PubMed-7670463;
 RA Murekanti Y., Natton M., Hagihara H., Shidata T., Ozawa M.,
 RA Sasanuma S.-I., Sasanuma M., Tsuchiya Y., Soeda E., Yokoyama K.,
 RA Yamazaki M., Tashiro H., Eki T.;
 RT Analysis of the nucleotide sequence of chromosome VI from
 RT Saccharomyces cerevisiae*.
 RL Nat. Genet. 10:261-268(1995).
 RN [2]
 RP SEQUENCE FROM N.A. AND CHARACTERIZATION.
 RX MEDLINE-97265402; PubMed-9111339;
 RA Vidan S., Mitchell A.P.;
 RT Stimulation of yeast meiotic gene expression by the
 RT glucose-repressible protein kinase Rlm15p*.
 RL Mol. Cell. Biol. 17:2688-2697(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Reinders A., Buerckert N., Boller T., Wlenken A., de Virgilio C.;
 RT Saccharomyces cerevisiae cAMP-dependent protein kinase controls entry
 RT into stationary phase through the Rlm15p protein kinase*.
 RL Submitted (Aug-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: INVOLVED IN THE ACTIVATION OF A MEIOTIC GENES ACTIVATION
 CC PATHWAY.
 CC -1- PTM: AUTOPHOSPHORYLATED.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC STRONG, WITH S.POMBE CER1.
 CC -1- SIMILARITY: CONTAINS 1 RESPONSE REGULATORY DOMAIN.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL: D50617; BAA09206.1; -
 CC EMBL: U83459; AAB64088.1; -
 CC EMBL: AJ001030; CAA04486.1; -
 CC HSSP: Q16539; IMFC.
 DR SCD: S0001861; RIM15.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR000961; Pkinase_C.
 DR InterPro: IPR001789; Response_reg.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00069; Pkinase; 2.
 DR Pfam: PF00072; response_reg; 1.
 DR SMART: SM00448; REC; 1.
 DR SMART: SM00133; S_TK_X; 1.
 DR SMART: SM00220; S_TKc; 1.

DR PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00110; RESPONSE_REGULATORY; 1.
KW Transferred; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation; Melosis.
FT DOMAIN 794 1254
FT DOMAIN 1636 1750
FT DOMAIN 343 358
FT DOMAIN 620 624
FT NP_BIND 800 808
FT BINDING 823 823
FT ACT_SITE 918 918
FT DOMAIN 975 980
FT DOMAIN 1213 1218
FT DOMAIN 1386 1391
SQ SEQUENCE 1770 AA; 196530 MW; DC1064825000FAFF CRC64;

Query Match 58.3%; Score 56; DB 1; Length 1770;
Best Local Similarity 64.3%; Pred. No. 1.5;
Matches 9; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 2 SEDEEHITDTE 15
I:|||||:|:|:
Db 1754 SQDEEHITLSDS 1767

RESULT 4
CNG4_BOVIN STANDARD; PRT; 1394 AA.
AC Q28181; Q28082; Q03861;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 240 kDa protein of rod photoreceptor CNG-channel [Contains: Glutamic acid-rich protein (GARP); Cyclic-nucleotide-gated cation channel 4 (CNG channel 4) (CNG-4) (Cyclic nucleotide-gated cation channel modulatory subunit)].
GN CNGB1 OR CNGG4.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RX MEDLINE=96009859; PubMed=7546742;
RA Koerschen H.G., Illing M., Seifert R., Sesti F., Williams A., Gotzes S., Colville C., Mueller F., Dose A., Godde M., Molday L., Kaupp U.B., Molday R.S.;
RA "A 240 kDa protein represents the complete beta subunit of the cyclic nucleotide-gated channel from rod photoreceptor.";
RL Neuron 15:627-636(1995).
RN [2]
RP SEQUENCE OF 454-1394 FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=96198098; PubMed=8626431;
RA Biel M., Zong X., Ludwig A., Sauter A., Hofmann F.;
RT "Molecular cloning and expression of the modulatory subunit of the cyclic nucleotide-gated cation channel.";
RL J. Biol. Chem. 271:6349-6355(1996).
RN [3]
RP SEQUENCE OF 1-590 FROM N.A.
RC TISSUE=Retina;
RA Sugimoto Y., Yatsunami K., Tsujimoto M., Khorana H.G., Ichikawa A.;
RL Submitted (XXX-1991) to the EMBL/GenBank/DBJ databases.
CC -1- SUBUNIT: FORMS FUNCTIONAL HETEROLOGIC CHANNELS WITH CNG3.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS: CNG4C (SHOWN HERE), CNG4D AND CNG4E; ARE PRODUCED BY ALTERNATIVE SPLICING. CNG4D IS BY FAR THE MOST FREQUENT FORM (CNG4C:CNG4E = 20:2:1) IN TESTIS.
CC -1- TISSUE SPECIFICITY: RETINA, TESTIS, KIDNEY, HEART, AND BRAIN.

-1- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE-GATED CATION CHANNEL FAMILY.
CC
CC
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CC
CC
CC EMBL; X89626; CAA61769.1; -
CC EMBL; X94707; CAA64367.1; -
CC EMBL; M61185; AAA30536.1; -
DR InterPro: IPR000638; Cation_chan_non_lig.
DR InterPro: IPR000595; cNMP_binding.
DR Pfam; PF00027; cNMP_binding; 1.
DR Pfam; PF00520; Ion_trans; 1.
DR SMART; SM00100; cNMP; 1.
DR PROSITE; PS00888; cNMP_BINDING_1; 1.
DR PROSITE; PS00889; cNMP_BINDING_2; 1.
DR PROSITE; PS00042; cNMP_BINDING_3; 1.
KW Ionic channel; Ion transport; CAMP-binding; Transmembrane;
KW Multigene family; Alternative splicing.
FT CHAIN 1 590
FT CHAIN 454 1394
FT DOMAIN 1 767
FT TRANSMEM 768 786
FT DOMAIN 787 800
FT TRANSMEM 801 819
FT DOMAIN 821 844
FT TRANSMEM 845 864
FT DOMAIN 865 901
FT TRANSMEM 902 924
FT DOMAIN 925 968
FT TRANSMEM 969 988
FT DOMAIN 989 1072
FT TRANSMEM 1073 1093
FT DOMAIN 1094 1394
FT NP_BIND 1081 1219
FT BINDING 1141 1141
FT BINDING 1153 1153
FT CARBOHYD 1067 1067
FT VARSPLIC 515 532
FT VARSPLIC 522 530
FT CONFLICT 341 341
FT CONFLICT 454 465
FT CONFLICT 482 482
FT CONFLICT 499 499
FT CONFLICT 572 590
FT CONFLICT 1283 1283
FT CONFLICT 1289 1289
FT CONFLICT 1336 1336
FT CONFLICT 1338 1338
SQ SEQUENCE 1394 AA; 155054 MW; EE6DA559BE3744A7 CRC64;

Query Match 51.0%; Score 49; DB 1; Length 1394;
Best Local Similarity 38.9%; Pred. No. 13;
Matches 7; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 DSEDEEHITITDTELP 18
I:|:|:|:|:|:|:|:
Db 459 DEEEQHSHVLLDSYLP 476

RESULT 5
IPHL_YEAST STANDARD; PRT; 1085 AA.
ID IPHL_YEAST
AC P39520;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update).

DT 01-OCT-1996 (Rel. 34, Last annotation update)

DE IFH1 protein (RRP3 protein)

CN IFH1 OR RRP3 OR YLR233C OR U8083.9.

OS Saccharomyces cerevisiae (Baker's yeast).

CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

CC Saccharomycetales; Saccharomycetaceae; Saccharomyces.

OX NCBI_TaxID=4932;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=FL100;

RX MEDLINE=95304839; PubMed=7785326;

RA Chered I., Thuriaux P.

RT "The IFH1 gene product interacts with a fork head protein in

RT Saccharomyces cerevisiae.";

RL yeast 148261-270(1995).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=S288C / AB972;

RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,

RA Favella A., Fulton L., Gattung S., Greco T., Kirsten J.,

RA Kucaba T., Hallsworth K., Hawkins J., Hillier L., Jier M.,

RA Johnson D., Johnston L., Langston Y., Latreille P., Le T.,

RA Madis E., Meneses S., Miller N., Nhan M., Pauley A., Peluso D.,

RA Ritten L., Riles L., Tatch A., Trevasis E., Vignati D.,

RA Wilcox L., Mohlman P., Vaudin M., Wilson R., Waterston R.

RL Submitted (DEC-1994) to the EMBL/Genbank/DBJ databases.

CC -1- FUNCTION: CONTROLS THE PRE-RRNA PROCESSING MACHINERY IN

CC CONJUNCTION WITH FHL1. COULD CONVERT FHL1 FROM A REPRESSOR

CC TO AN ACTIVATOR.

CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).

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CC -----

DR EMBL: Z29488; CA82624.1; -

DR EMBL: U19027; AAB67412.1; -

DR PIR: S47477; S47477.

DR SCD: S0004213; IFH1.

KM Nuclear protein; transcription regulation.

FT DOMAIN 122 163 ASP/GLU-RICH (HIGHLY ACIDIC).

SO SEQUENCE 1085 AA; 122491 MW; BEIC/DEF06213FE0 CRC64;

Query Match 50.0%; Score 48; DB 1; Length 1085;

Best Local Similarity 47.1%; Pred. NO. 14;

Matches 8; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 DSEDEDEHTITITPELP 17

DB 404 DEDEDEDEIMSDPMP 420

RESULT 6

FBL2_MOUSE STANDARD; PRT; 1221 AA.

AC P37889; O9WU12; 30, Created)

DT 01-OCT-1994 (Rel. 30, Last sequence update)

DT 01-OCT-1994 (Rel. 30, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Fibulin-2 precursor.

GN FBLN2

OS Mus musculus (Mouse).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A., AND SEQUENCE OF 27-35.

RC TISSUE=Fibroblast;

RX MEDLINE=94064787; PubMed=8245130;

RA Pan T.-C., Sasaki T., Zhang R.-Z., Faessler R., Timpl R., Chu M.-L.;

RT "Structure and expression of fibulin-2, a novel extracellular matrix

RT protein with multiple EGF-like repeats and consensus motifs for

RT calcium binding."

RT J. Cell Biol. 123:1269-1277(1993).

RN [2]

RP SEQUENCE FROM N.A.

RC MEDLINE=99337686; PubMed=10406956;

RX Graessel S., Sicot F.-X., Gotta S., Chu M.-L.;

RT "Mouse fibulin-2 gene. Complete exon-intron organization and promoter

RT characterization."

RT Eur. J. Biochem. 263:471-477(1999).

CC -1- FUNCTION: ITS BINDING TO FIBRONECTIN AND SOME OTHER LIGANDS IS

CC CALCIUM DEPENDENT.

CC -1- SUBUNIT: HOMOTRIMER; DISULFIDE-LINKED.

CC -1- SUBCELLULAR LOCATION: Extracellular matrix.

CC -1- ALTERNATIVE PRODUCTS: AT LEAST TWO FORMS OF FIBULIN-2 DUE TO THE

CC PRESENCE OR ABSENCE OF A SINGLE EGF-LIKE (3) REPEAT MAY ARISE BY

CC ALTERNATIVE SPLICING.

CC -1- TISSUE SPECIFICITY: COMPONENT OF BOTH BASEMENT MEMBRANES AND OTHER

CC CONNECTIVE TISSUES.

CC -1- SIMILARITY: CONTAINS 3 ANAPHYLATOXIN-LIKE DOMAINS.

CC -1- SIMILARITY: CONTAINS 11 EGF-LIKE DOMAINS.

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CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL: X75285; CA53040.1; -

DR EMBL: AF135253; AAD34456.1; -

DR EMBL: AF135239; AAD34456.1; JOINED.

DR EMBL: AF135240; AAD34456.1; JOINED.

DR EMBL: AF135241; AAD34456.1; JOINED.

DR EMBL: AF135242; AAD34456.1; JOINED.

DR EMBL: AF135243; AAD34456.1; JOINED.

DR EMBL: AF135244; AAD34456.1; JOINED.

DR EMBL: AF135245; AAD34456.1; JOINED.

DR EMBL: AF135246; AAD34456.1; JOINED.

DR EMBL: AF135247; AAD34456.1; JOINED.

DR EMBL: AF135248; AAD34456.1; JOINED.

DR EMBL: AF135249; AAD34456.1; JOINED.

DR EMBL: AF135250; AAD34456.1; JOINED.

DR EMBL: AF135251; AAD34456.1; JOINED.

DR EMBL: AF135252; AAD34456.1; JOINED.

DR PIR: A49457; A49457.

DR HSSP: P07204; IFGD.

DR MGD: M61:95488; FBLN2.

DR InterPro: IPR000020; Anaphylatoxin.

DR InterPro: IPR000152; Asx_hydroxyl.

DR InterPro: IPR000561; EGF-like.

DR InterPro: IPR001881; EGF-Ca.

DR Pfam: PF01821; ANATO; 2.

DR Pfam: PF00008; EGF; 6.

DR SMART: SM00104; ANATO; 3.

DR SMART: SM00179; EGF_CA; 9.

DR SMART: SM00001; EGF_Like; 2.

DR PROSITE: PS00010; ASX_HYDROXYL; 5.

DR PROSITE: PS01177; ANAPHYLATOXIN_1; 3.

DR PROSITE: PS01178; ANAPHYLATOXIN_2; 3.

DR PROSITE: PS00022; EGF_1; FALSE_NEG.

DR PROSITE: PS01186; EGF_2; 5.

DR PROSITE: PS01187; EGF_CA; 10.

KM Signal; Glycoprotein; Extracellular matrix; Plasma; EGF-like domain;

KW Calcium-binding; Alternative splicing; Repeat.

FT SIGNAL 1 26

FT CHAIN 27 1221 FIBULIN-2.

FT DOMAIN 27 434 N.

FT SUBDOMAIN 27 176 SUBDOMAIN NA (CYS-RICH).

Query Match	49.5%;	Score 47.5;	DB 1;	Length 1221;	DR
Best Local Similarity	50.0%;	Pred. No. 19;			KW
Matches 9;	Conservative 4;	Mismatches 2;	Indels 3;	Gaps 1;	Signal
Qy 1 DSEDEEHFTITDELPP 18					FT SIGNAL 1 24
	1111111111				FT CHAIN 25 300
	1111111111				FT DOMAIN 50 100
Db 274 DEEEETLVT---EP 288					FT DOMAIN 121 171
					FT
					FT

FT DOMAIN 213 263 BPTI/RUNITE INHIBITOR 3
(BY SIMILARITY).
FT DISULFID 50 100 BY SIMILARITY.
FT DISULFID 59 83 BY SIMILARITY.
FT DISULFID 75 96 BY SIMILARITY.
FT ACT SITE 60 61 REACTIVE BOND (BY SIMILARITY).
FT DISULFID 121 171 BY SIMILARITY.
FT DISULFID 130 154 BY SIMILARITY.
FT DISULFID 146 167 BY SIMILARITY.
FT ACT SITE 131 132 REACTIVE BOND (BY SIMILARITY).
FT DISULFID 213 263 BY SIMILARITY.
FT DISULFID 222 246 BY SIMILARITY.
FT ACT SITE 223 259 BY SIMILARITY.
FT ACT SITE 223 224 REACTIVE BOND (BY SIMILARITY).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 191 191 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 252 252 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 31 31 MISSING (IN REF. 3).
FT CONFLICT 269 272 PKSI -> RNL5 (IN REF. 3).
SO SEQUENCE 300 AA: 34435 MM: A08DE36537708CA6 CRC64;

Query Match 49.0%; Score 47; DB 1; Length 300;
Best Local Similarity 62.5%; Pred. No. 4.5; Mismatches 0;
Matches 10; Conservative 2; Indels 0; Gaps 0;

OY 2 SEDEHITITDTEL 17
:|||||:|:|:|
DB 26 AEDEEFTNITDIKPP 41

RESULT 8
IP3T_RAT IP3T_RAT STANDARD; PRT: 2670 AA.
AC 063269;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE inositol 1,4,5-trisphosphate receptor type 3 (Type 3 inositol 1,4,5-
trisphosphate receptor) (Type 3 insp3 receptor) (IP3 receptor isoform
3) (insp3R3) (IP3R-3).
GN ITPR3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9326594; PubMed=8388391;
RA Blondel O., Takeda J., Janssen H., Setno S., Bell G.I.;
RT "Sequence and functional characterization of a third inositol
trisphosphate receptor subtype, IP3R-3, expressed in pancreatic
islets, kidney, gastrointestinal tract, and other tissues.";
RT J. Biol. Chem. 268:11355-11363(1993).
RL
CC -1- FUNCTION: RECEPTOR FOR INOSITOL 1,4,5-TRISPHOSPHATE, A SECOND
MESSENGER THAT MEDIATES THE RELEASE OF INTRACELLULAR CALCIUM.
CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC -1- SUCCELLULAR LOCATION: Integral membrane protein. Endoplasmic
reticulum (BY SIMILARITY).
CC -1- DOMAIN: THE RECEPTOR CONTAINS A CALCIUM CHANNEL IN ITS C-TERMINAL
EXTREMITY. ITS LARGE N-TERMINAL CYTOPLASMIC REGION HAS THE LIGAND-
BINDING SITE IN THE N-TERMINUS AND MODULATORY SITES IN THE MIDDLE
PORTION IMMEDIATELY UPSTREAM OF THE CHANNEL REGION.
CC -1- PTM: PHOSPHORYLATED ON TYROSINE RESIDUES (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE INSP3 RECEPTOR FAMILY.
CC
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or send an email to license@isb-sib.ch).

CC EMBL, L06096; AAA41446.1;
DR InterPro: IPR000636; Cation_chan_non_11g.
DR InterPro: IPR001682; Channel_pore_Ca_Na.
DR InterPro: IPR000493; Insp3_bind_receptor.
DR InterPro: IPR003608; MIR.
DR InterPro: IPR000699; RYDR_ITPR.
DR Pfam: PF00520; Ion_trans_1.
DR Pfam: PF01365; RYDR_ITPR_1.
DR PRINTS: PR00779; INSP3RCPTPR.
DR SMART: SM00472; MIR; 4.
KW Receptor; Transmembrane; Phosphorylation; Endoplasmic reticulum;
KW Ionic channel; Ion transport; Calcium channel;
KW DOMAIN 1 2201 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 2202 2222 POTENTIAL.
FT TRANSMEM 2223 2233 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 2234 2254 POTENTIAL.
FT TRANSMEM 2255 2263 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 2264 2284 POTENTIAL.
FT TRANSMEM 2285 2324 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 2325 2345 POTENTIAL.
FT TRANSMEM 2346 2367 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 2368 2388 POTENTIAL.
FT TRANSMEM 2389 2495 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 2496 2516 POTENTIAL.
FT TRANSMEM 2517 2670 POTENTIAL.
FT MOD_RES 2582 2582 PHOSPHORYLATION (POTENTIAL).
FT MOD_RES 2582 2582 PHOSPHORYLATION (POTENTIAL).
SO SEQUENCE 2670 AA: 304284 MM: 13C787E4C2886E45 CRC64;

Query Match 47.9%; Score 46; DB 1; Length 2670;
Best Local Similarity 53.8%; Pred. No. 80;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 4 EDEHITITDTEL 16
:|||||:|:|:|
DB 957 EDNEHTVMEKTL 969

RESULT 9
CP3I_RAT CP3I_RAT STANDARD; PRT: 504 AA.
AC P04800; Q64580;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Cytochrome P450 3A1 (EC 1.14.14.1) (CYP3A1) (P450-PCN1).
GN CYP3A1 OR CYP3A-1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85207783; PubMed=3838989;
RA Gonzalez F.J., Nebert D.W., Hardwick J.P., Kasper C.B.;
RT "Complete cDNA and protein sequence of a pregnenolone 16 alpha-
carbonitrile-induced cytochrome P-450. A representative of a new gene
family.";
RT J. Biol. Chem. 260:7435-7441(1985).
RL
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MISTAR; TISSUE=LIVER;
RX MEDLINE=92117688; PubMed=1731631;
RA Ribet V., Lechner M.C.;
RT "Cloning and characterization of a novel CYP3A1 allelic variant:
analysis of CYP3A1 and CYP3A2 sex-hormone-dependent expression reveals
that the CYP3A2 gene is regulated by testosterone.";
RT Arch. Biochem. Biophys. 293:147-152(1992).
RN [3]
RP SEQUENCE OF 1-24 FROM N.A.
RX MEDLINE=92196074; PubMed=1372436;
RX Burger H.J., Schuetz J.D., Schuetz E.G., Guzelian P.S.;

Query Match	45.8%	Score 44:	DB 1:	Length 504;
Best Local Similarity	43.8%	Pred. No. 24;		
Matches 7;	Conservative	5;	Mismatches	4;
			Indels	0;
			Gaps	0;

RESULT	10
TRAIL_MOUSE	
ID	TRAIL_MOUSE
STANDARD;	PRT; 706 AA..

AC	Q9CQNL1;	DT	DT	DT	DT	DT	DT
01-MAR-2002	(Rel. 41, Created)						
01-MAR-2002	(Rel. 41, Last sequence update)						
01-MAR-2002	(Rel. 41, Last association update)						

DE Heat shock protein 70 kDa, mitochondrial precursor (HSP 75) (Tumor
DE necrosis factor type I receptor associated protein) (TRAP-1) (TNF-
DE associated protein 1).

GN
OS
OC
OC
TRAPI.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutaria; Rodentia;
Sciuridae; Muridae.

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=1009;
 [1]
 RN SEQUENCE FROM N.A.
 RP

RC STRAIN-C57BL/6J; TISSUE-Embryonic stem cells, and Kidney;
RX MEDLINE-21085660; Pubmed-11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RX Nishida K. "Effect of the combination of a

RA Alakawa I., Nara A., Fukunishi I., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

CC	EMBL; AK010341; BAB26865.1; -
DR	EMBL; AK002409; BAB22078.1; -
DR	HSSP; P07900; 1YER.

DR MGD: MGI:1915265; Trap1.
DR InterPro: IPR003594; HATPase_c.
DR InterPro: IPR001404; HSP90.
DR Pfam: PF02518; HATPase_c.1

DR Pcam; PR00183; HSP90; 3.
DR PRINTS; PR00775; HEATSHOCK90.
DR SMART; SM00387; HATPase_c; 1.

DR	PROSITE; PS00298; HSP90; FALSE NEG.
KW	Chaperone; ATP-binding; Mitochondrion; Transit peptide.
FT	TRANSIT 1 206 MITOCHONDRION (POTENTIAL).
ET	CHAIN 2 706 HEAT SHOCK PROTEIN 75 KDA

SQ SEQUENCE 706 AA; 80208 MW; 7183CE538CB36464 CRC64;

Query Match	45.8%;	Score 44;	DB 1;	Length 706;
Best Local	Similarity 53.3%;	pred. No. 35;		
Matches 8;	Conservative	4;	Mismatches	
		3;	Indels	0; Gaps 0;

QY	1 DSEDEEHYITDE 15
DB	67 DKEESLHSIISTE 81

RESULT 11
M2C M01SE

M3KC_MOUSE	STANDARD;	PRT;	888 AA.
ID M3KC_MOUSE			
AC Q60700;	P70286;		
DT 16-OCT-2001	Rel. 40, Created		

DT 16-OCT-2001 (Rel. 4.0, Last sequence update)
DT 01-MAR-2002 (Rel. 4.1, Last annotation update)
DT DT
DE Mitogen-activated protein kinase kinase kinase 12 (EC 2.7.1.37)
DE Mitogen-activated protein kinase kinase kinase 12 (EC 2.7.1.37)
DE Mitogen-activated protein kinase kinase kinase 12 (EC 2.7.1.37)

DE (Leucine zipper protein kinase). (ZPK) (Dual leucine zipper bearing
DE kinase) (DLK).
DE MAP3K12 OR ZPK.
OS MUS musculus (Mouse).
OS

OC Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata;
OC Mammalia; Eutheria; Rodentia;
OX Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;

111
RN
RP
SEQUENCE FROM N.A.

CC STAIN-CD-1; TISSUE-Brain;
RX MEDLINE-95074107; Pubmed-7983011;
RA Holzman L.B., Merritt S.E., Fan G.;
RT Identification, molecular cloning, and characterization of dual
leucine zipper bearing kinase. A novel serine/threonine protein kinase
that defines a second subfamily of mixed lineage kinases.";
RT J. Biol. Chem. 269:30808-30817(1994).
RN [2]
RP SEQUENCE FROM N/A.
RC STRAIN-ICR/Swiss Webster; TISSUE-Brain;
RX MEDLINE-96365388; Pubmed-8769565;
RA Blount R., Beaudoin J., Bergeron P., Nadeau A., Grondin G.;
RT "Cell-specific expression of the ZPK gene in adult mouse tissues.";
RT DNA Cell Biol. 15:631-642(1996).
RN [3]
RP PHOSPHORYLATION OF MAPK12, AND MUTAGENESIS OF LYS-185 AND GLU-192.
RX MEDLINE-96279269; Pubmed-8663324;
RA Meta M., Merritt S.E., Fan G., Yu G.G., Holzman L.B.;
RT Characterization of dual leucine zipper-bearing kinase, a mixed
lineage kinase present in synaptic terminals whose phosphorylation
state is regulated by membrane depolarization via calcineurin.";
RT J. Biol. Chem. 271:16888-16896(1996).
CC -1- FUNCTION. May be an activator of the JNK/SAPK pathway.
CC Phosphorylates beta-casein, histone 1 and myelin basic protein in
CC vitro.
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a. phosphoprotein.
CC -1- COFACTOR: Magnesium.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic and membrane-associated.
CC -1- TISSUE SPECIFICITY: Expressed in brain, kidney, lung, heart,
CC testis, gastrointestinal tract, stomach, liver and pancreas.
CC Within the nervous system, predominantly expressed in neurons and
CC enriched in synaptic terminals.
CC -1- PIM: Autophosphorylated on Ser/Thr. Phosphorylated in cytosol
CC under basal conditions and dephosphorylated when membrane-
CC associated.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MAP KINASE KINASE SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U14636; AAA57280.1; -;
DR EMBL; U23789; AAB17123.1; -;
DR HSSP; P06213; IIRK.
DR MGD; MGI:1346881; Mapk12.
DR InterPro; IPR000719; Euk_Pkinase.
DR InterPro; IPR004040; Sty_Pkinase.
DR InterPro; IPR002290; Ser_Thr_Pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR SMART; SM00221; STYK; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; FALSE_NEG.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR TransEnzyme; Serine/threonine-protein kinase; ATP-binding;
KM Phosphorylation; Magnesium; Membrane.
RV DOMAIN 158 399
FT NP_BIND 164 172
FT BINDING 185 185
FT ACT_SITE 269 269
FT ACT_SITE 56 62
FT DOMAIN 668 671
FT DOMAIN 698 701
FT DOMAIN 753 758
FT MUTAGEN 185 185
FT MUTAGEN 192 192
FT CONFLICT 18 18
FT CONFLICT 28 29
FT CONFLICT 382 382
FT CONFLICT 382 382
FT K L -> N (1N REF. 2).
FT S -> T (1N REF. 2).
FT

```

FT CONFLICT 494 495 EO -> DE (IN REF. 2).
FT CONFLICT 517 N -> D (IN REF. 2).
FT CONFLICT 794 794 E -> G (IN REF. 2).
SQ SEQUENCE 888 AA; 96083 MW; CEECF1D34FF89A8B CRC64;

Query Match 45.8%; Score 44; DB 1; Length 888;
Best Local Similarity 47.1%; Pred. No. 46;
Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

OY 2 SEDEDEHTITDTELP 18
1:11 : : 1111
Db 751 SSEECEGEVDESELP 767

RESULT 12
MKRC_RAT STANDARD: PRT; 888 AA.
AC Q63796;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Mitogen-activated protein kinase kinase kinase 12 (EC 2.7.1.37)
DE (MAPK upstream kinase) (MUK).
GN MAP3K12 OR MUK.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RX NCBI_TaxID=10116;
[1]
RA SEQUENCE FROM N.A.
RA MEDLINE=96226099; PubMed=8637721;
RA Hirai S., Izawa M., Osada S., Spyrou G., Ohno S.;
RT Activation of the JNK pathway by distantly related protein kinases,
RT MEK and MUK."
RL Oncogene 12:641-650(1996).
CC -1- FUNCTION: May be an activator of the JNK/SAPK pathway.
CC phosphorylates beta-casein, histone 1 and myelin basic protein in
CC vitro.
CC -1- CATALYTIC ACTIVITY: ATP + a protein - ADP + a phosphoprotein.
CC -1- COFACTOR: Magnesium.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic and membrane-associated (By
CC similarity).
CC -1- PRT: Autophosphorylated on Ser/Thr. Phosphorylated in cytosol
CC under basal conditions and dephosphorylated when membrane-
CC associated (By similarity).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MAP KINASE KINASE KINASE SUBFAMILY.
CC -----
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CC -----
CC EMBL: D49785; BAA08621.1; -
DR HSPF; P06213; IIRK.
DR InterPro: IPR000719; Euk_Pkinase.
DR InterPro: IPR004040; STY_Pkinase.
DR InterPro: IPR002290; Ser_thr_Pkinase.
DR Pfam: PF00069; Pkinase; 1.
DR SMART: SM00221; STYK; 1.
DR PROSITE, PS00107; PROTEIN_KINASE_ATP_FALSE_NEG.
DR PROSITE, PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE, PS50011; PROTEIN_KINASE_DOM; 1.
KW Transferrase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation; Magnesium; Membrane.
FT DOMAIN 158 399 PROTEIN KINASE.
FT NP_BIND 164 172 ATP (BY SIMILARITY).
FT BINDING 185 185 ATP (BY SIMILARITY).
FT ACT_SITE 269 269 BY SIMILARITY.

```

Query Match

Best Local Similarity 46.7%; Pred. No. 1.3e+02;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 1 DSEDEHHITITDTE 15
DB 548 DDEDEDDQMLVDSE 562

RESULT 14

GATB.METH STANDARD; PRT: 449 AA.
ID GATB.METH 027341;
AC 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable glutamyl-TRNA(Gln) amidotransferase subunit B (EC 6.3.5.-)
GN (Glu-ADT subunit B).
OS Methanobacterium thermoautotrophicum.
OC Archaea: Euryarchaeota: Methanobacteriales: Methanobacteriaceae:
OC Methanobacter.
OX NCBI_TaxID=145262;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN-DELTA H;
RX MEDLINE=98037514; PubMed=9371463;
RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
RA Adrege T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
RA Harrison D., Hoang L., Keagle P., Lunn W., Pothier B., Qiu D.,
RA Spadefora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
RA Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
RA McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
RA Daniels C.J., Mo J.-I., Rice P., Noelling J., Reeve J.N.;
*Complete genome sequence of Methanobacterium thermoautotrophicum
delta: functional analysis and comparative genomics.
RT Bacteriol. 179:7135-7152(1997).
RL
CC -1- FUNCTION: FURNISHES A MEANS FOR FORMATION OF CORRECTLY CHARGED
CC GAN-TRNA(Gln) THROUGH THE TRANSMUTATION OF MISACLYATED GLU-
CC TRNA(Gln) IN ORGANISMS WHICH LACK GLUTAMINYL-TRNA SYNTHETASE. THE
CC REACTION TAKES PLACE IN THE PRESENCE OF GLUTAMINE AND ATP THROUGH
CC AN ACTIVATED GAMMA-PHOSPHO-GLU-TRNA(Gln) (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: ATP + L-GLUTAMINYL-TRNA(Gln) + L-GLUTAMINE - ADP
CC + PHOSPHATE + L-GLUTAMINYL-TRNA(Gln).
CC -1- SUBUNIT: HETEROMER OF A, B AND C SUBUNITS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE GATB FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: AE000893; AAB85762.1;
DR InterPro: IPR003789; DUF186.
DR InterPro: IPR001773; Gln_amidotransf_B.
DR Pfam: PF02637; DUF186; 1.
DR Pfam: PF02934; GATB_N; 1.
DR PROSITE: PS01234; GATB; 1.
KW Protein biosynthesis; Ligase; Complete proteome.
SQ SEQUENCE 449 AA: 51131 MW: 722812F7E5B5F1 CAC64;

Query Match

Best Local Similarity 44.8%; Score 43; DB 1; Length 449;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 3 EDEDEHHITITDTE 18
DB 240 EEAEDYRIIPDPLP 255

RESULT 15
ID INGR_HUMAN STANDARD; PRT: 489 AA.
AC P15260;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Interferon-gamma receptor alpha chain precursor (CDw119).
GN IFNGR1.
OS Homo sapiens (Human).
OC Eukaryota: Metazoa: Chordata: Vertebrata: Euteleostomi;
OC Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=89003065; PubMed=2971451;
RX Aguet M., Dembic Z., Meriin G.;
RT Molecular cloning and expression of the human interferon-gamma
RT receptor.*
RL Cell 55:273-280(1988).
[2]
RN SEQUENCE FROM N.A.
RP Philimore B.;
RL Submitted (JUL-1999) to the EMBL/Genbank/DBJ databases.
[3]
RN DISULFIDE BONDS, PARTIAL SEQUENCE, AND MUTAGENESIS.
RX MEDLINE=93183911; PubMed=8443182;
RA Stueber D., Friedlein A., Pountoulakis M., Lahm H.-W., Garotta G.;
RT Alignment of disulfide bonds of the extracellular domain of the
RT interferon gamma receptor and investigation of their role in
RT biological activity.*
RL Biochemistry 32:2423-2430(1993).
[4]
RN X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 26-248.
RX MEDLINE=95342235; PubMed=7617032;
RA Walter M.R., Windsor W.T., Nagabhushan T.L., Lundell D.J., Lunn C.A.,
RA Zaudy P.J., Narula S.K.;
RT Crystal structure of a complex between interferon-gamma and its
RT soluble high-affinity receptor.*
RL Nature 376:230-235(1995).
[5]
RN X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 28-122 IN COMPLEX WITH
RN ANTI-BODY.
RX MEDLINE=98035727; PubMed=9367779;
RA Sogabe S., Stuart F., Henke C., Bridges A., Williams G., Birch A.,
RA Winkler F.K., Robinson J.A.;
RT Neutralizing epitopes on the extracellular interferon gamma receptor
RT (IFN-gamma) alpha-chain characterized by homolog scanning mutagenesis
RT and X-ray crystal structure of the A6 fab-IFN-gammaRI-108 complex.*
RL J. Mol. Biol. 273:882-897(1997).
[6]
RN X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF COMPLEX WITH ING.
RX MEDLINE=20444407; PubMed=10986460;
RA Thiel D.J., le Du M.-H., Walter R.L., D'Arcy A., Chene C.,
RA Pountoulakis M., Garotta G., Winkler F.K., Falick S.E.;
RT Observation of an unexpected third receptor molecule in the crystal
RT structure of human interferon-gamma receptor complex.*
RL Structure 8:927-936(2000).
CC -1- FUNCTION: RECEPTOR FOR INTERFERON GAMMA. TWO RECEPTORS BIND ONE
CC INTERFERON-GAMMA DIMER.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- PTM: PHOSPHORYLATED AT SER/THR RESIDUES.
CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC -1- DATABASE: NAME-PROW; NOTE-CD guide CDw119 entry;
CC WWW=<http://www.ncbi.nlm.nih.gov/prov/cd/cdw119.htm>.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----

DR EMBL; J03143; AAA52731.1; -
DR EMBL; AL050337; CAB53062.1; -
DR PIR; A31555; A31555.
DR PDB; 1JRH; 25-MAR-98.
DR PDB; IFG9; 11-AUG-00.
DR GlycoSuiteDB; P15260; -
DR MIM; 107470; -
DR MIM; 209950; -
DR InterPro; IPR000282; Cytok_receptor_2.
KW Receptor, transmembrane; Glycoprotein; Signal; Phosphorylation;
KW Immunoglobulin domain; 3D-structure.
FT SIGNAL 1 17
FT CHAIN 18 489 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN.
FT DOMAIN 18 245 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 246 266 POTENTIAL.
FT DOMAIN 267 489 CYTOPLASMIC (POTENTIAL).
FT DISULFID 77 85
FT DISULFID 122 167
FT DISULFID 195 200
FT DISULFID 214 235
FT CARBOHYD 34 34 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 79 79 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 179 179 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 240 240 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 489 AA; 54404 MW; DCF9E574D8F47400 CRC64;

Query Match 44.8%; Score 43; DB 1; Length 489;
Best Local Similarity 44.4%; Pred. No. 33;
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
OY 1 DSEDEHTIITDTEPP 18
||| | | | | | | |
Db 415 DSCLESLSLSDSEFP 432

Search completed: September 20, 2002, 10:32:02
Job time: 235 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 20, 2002, 10:27:18 : Search time 25.08 seconds
(without alignments)
124.159 Million cell updates/sec

Title: US-08-854-764-7

Perfect score: 96
Sequence: 1 DSEDEHHTITDTLELP 18

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 562222 seqs, 17294929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: 1: SPREMBL_19:*

- 2: sp.archaea:*
- 3: sp.bacteria:*
- 4: sp.fungi:*
- 5: sp.human:*
- 6: sp.invertebrate:*
- 7: sp.mammal:*
- 8: sp.mhc:*
- 9: sp.organelle:*
- 10: sp.phage:*
- 11: sp.plant:*
- 12: sp.podent:*
- 13: sp.virus:*
- 14: sp.vertebrate:*
- 15: sp.unclassified:*
- 16: sp.virus:*
- 17: sp.bacteriap:*
- 17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	96	100.0	251	4	095103
2	55	57.3	2225	5	045881
3	51	53.1	873	4	09UKY1
4	51	53.1	873	11	P70121
5	50.5	52.6	224	4	000309
6	50.5	52.6	677	4	043863
7	50.5	52.6	1160	4	096Q28
8	50.5	52.6	1256	4	075085
9	50.5	52.6	1287	4	096Q29
10	50.5	52.6	1462	4	096Q27
11	49.5	51.6	526	4	096AG1
12	49	51.0	1044	12	091167
13	48	50.0	585	17	097806
14	47.5	49.5	1174	11	099K58
15	47	49.0	360	3	006810
16	47	49.0	1179	4	013545

17	47	49.0	1189	4	09UE80	09ue80 homo sapien
18	47	49.0	1189	4	000145	000145 homo sapien
19	47	49.0	2942	12	09WB76	09wb76 gb virus c
20	46	47.9	146	12	080931	080931 human papil
21	46	47.9	198	12	091G78	091g78 porcine ade
22	46	47.9	199	12	09W9X3	09w9x3 porcine ade
23	46	47.9	467	10	09FF99	09ff99 arabidopsis
24	45.5	47.4	412	10	09FT25	09ft25 arabidopsis
25	45	46.9	244	5	062156	062156 caenorhabd
26	45	46.9	259	16	066541	066541 aquifex aco
27	45	46.9	354	11	062509	062509 mus musculu
28	45	46.9	396	3	093955	093955 yarrowia 11
29	45	46.9	404	16	0928H4	0928h4 chlamydia p
30	45	46.9	455	11	062511	062511 mus musculu
31	45	46.9	504	4	096Q33	096q33 homo sapien
32	45	46.9	529	4	096Q74	096q74 homo sapien
33	45	46.9	570	4	096Q75	096q75 homo sapien
34	45	46.9	599	5	022089	022089 caenorhabd
35	45	46.9	638	12	091TL4	091tl4 tupala herp
36	45	46.9	762	5	09VXQ6	09vxq6 drosophila
37	44.5	46.4	471	5	020178	020178 caenorhabd
38	44	45.8	106	10	09S299	09s299 arabidopsis
39	44	45.8	163	11	070618	070618 mus musculu
40	44	45.8	170	6	09N0H2	09n0h2 dalaenopter
41	44	45.8	306	4	099848	099848 homo sapien
42	44	45.8	306	4	096A66	096a66 homo sapien
43	44	45.8	379	16	007527	007527 bacillus su
44	44	45.8	502	11	006884	006884 rattus norv
45	44	45.8	610	10	09L715	09l715 arabidopsis

ALIGNMENTS

RESULT 1

ID 095103 PRELIMINARY; PRT; 251 AA.

AC 095103:

DT 01-MAY-1999 (TEMBLrel. 10, Created)

DT 01-MAY-1999 (TEMBLrel. 10, Last sequence update)

DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)

DE TISSUE FACTOR PATHWAY INHIBITOR BETA (HYPOTHETICAL 28.7 KDA PROTEIN).

GN TPPIBETA.

OS Homo sapiens (human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_Taxid=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Chang J.-Y., Monroe D.M., Roberts H.R.:

RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RA Strausberg R., to the EMBL/GenBank/DBJ databases.

RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF021834; AAD01700.1; -

DR EMBL; BC015514; AAL15514.1; -

DR HSP; P10646; ITFX.

DR InterPro: IPR002223; Kunitz_BPTI.

DR Pfam: PF000014; Kunitz_BPTI.

DR PRINTS; PR00759; BASICPTASE.

DR SMART; SM00131; KU; 2.

DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.

DR PROSITE; PS02079; BPTI_KUNITZ_2; 2.

KW Serine protease inhibitor; Hypothetical protein.

SEQUENCE 251 AA; 28652 MW; 9B3F76A52B4F0B9 CRC64;

Query Match 100.0%; Score 96; DB 4; Length 251;
Best Local Similarity 100.0%; Pred. No. 8; le-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 1 DSEDEEHTIITDTELP 18
Db 29 DSEDEEHTIITDTELP 46

RESULT 2
O45881 PRELIMINARY; PRT; 2225 AA.
ID O45881;
AC O45881;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE W01F3.3 PROTEIN.
GN W01F3.3
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditiidae; Rhabditidae; Caenorhabditis.
OC Rhabditiidae; Pterodermidae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Cummings P.N.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RN none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; Z92815; CAB07294.1;
DR HSP; P31713; 1SHP
DR InterPro; IPR002899; EB.
DR InterPro; IPR002223; Kunitz_BPTI.
DR InterPro; IPR000716; Thyroglobulin_1.
DR Pfam; PF00014; Kunitz_BPTI_10.
DR Pfam; PF00086; thyroglobulin_1.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00131; KU; 10.
DR SMART; SM00211; TY; 1.
DR SMART; SM00289; WRI; 4.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 8.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 10.
DR PROSITE; PS00484; THYROGLOBULIN_1; UNKNOWN_1.
KW Serine protease inhibitor
SQ SEQUENCE 2225 AA; 242198 MW; A5DD8AE9D2A7B02A CRC64;

Query Match 57.3%; Score 55; DB 5; Length 2225;
Best Local Similarity 55.6%; Pred. No. 4.4;
Matches 10; Conservative 3; Mismatches 5; Indels 1

Qy 1 DSEDEEHTIITDTELP 18
Db 663 ETEDEEHAVTITPLAP 680

RESULT 3
Q9UKY1 PRELIMINARY; PRT; 873 AA.
ID Q9UKY1
AC Q9UKY1;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ZINC FINGER HOMEOBOX PROTEIN ZHX1 (ZHX1 PROTEIN).
GN ZHX1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA
RL
RX
RN
RT
RT TISSUE=LIVER.

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RX MEDLINE-99373128; PubMed-10441475;
RA Yamada K., Printz R.L., Osawa H., Granner D.K.;
RT "Human ZHX1: cloning, chromosomal location, and interaction with
RL transcription factor NF- $\kappa$ B."
RT Biochem. Biophys. Res. Commun. 261:614-621(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Mueller R., Ziegler B.L.;
RL "Identification and cloning of the human ZHX1 gene."
RT Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR ENBL; AF106862; AAD50624.1; -
DR ENBL; AF195766; AAF35183.1; -
DR TRANSFAC; T04355; -
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR000822; Znf-C2H2.
DR Pfam; PF00046; homeobox; 4.
DR Pfam; PF00096; zf-C2H2; 2.
DR SMART; SM00389; HOX; 5.
DR SMART; SM00355; Znf_C2H2; 2.
DR PROSITE; PS50071; HOMEBOX_2; 4.
DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 1.
DR DNA-binding; Homeobox; Nuclear protein; Zinc-finger.
KW KW
SQ SEQUENCE 873 AA; 98097 MW; 66CF1C8C5BF824E5 CRC64;

Query Match 53.1%; Score 51; DB 4; Length 873;
Best Local Similarity 61.1%; Pred. No. 7.4;
Matches 11; Conservative 1; Mismatches 6; Indels 0; Gaps

QY 1 DSEDEDEHTIITDTLPP 18
   I I I I I I I I I I I I
DB 844 DQEDREEDTSDTWERPP 861

RESULT 4
P70121
ID P70121 PRELIMINARY; PRT; 873 AA.
AC P70121;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE DNA-BINDING PROTEIN.
GN ZHX1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-996311380; PubMed-8713137;
RA Barthelemy I., Carramolino L., Gutierrez J., Barbero J.L., Marquez G.
RA "Zhx-1: A novel mouse homeodomain protein containing two zinc-fingers
RT and five homeodomains."
RL Biochem. Biophys. Res. Commun. 224:870-876(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Zaballos A.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR ENBL; Z54200; CAA90905.1; -
DR TRANSFAC; T04356; -
DR MGD; MGI:109271; Zhx1.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR000822; Znf-C2H2.
DR Pfam; PF00046; homeobox; 4.
DR Pfam; PF00096; zf-C2H2; 2.
DR SMART; SM00389; HOX; 5.
DR SMART; SM00355; Znf_C2H2; 2.
DR PROSITE; PS50071; HOMEBOX_2; 4.
DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 1.
DR DNA-binding; Zinc-finger.
SQ SEQUENCE 873 AA; 97621 MW; 831CDB694ADCFE4F CRC64;

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Query Match 53.1% Score 51; DB 11; Length 873;
Best Local Similarity 61.1% Pred. No. 7.4;
Matches 11; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Oy 1 DSEDEEHTITDTLPP 18
   1 11111 1 : 11 11
Db 844 DQSEDEEHTDSDFTWEP 861

RESULT 5
ID 000309 PRELIMINARY; PRT; 224 AA.
AC 000309;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE WMP3 (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
RP MEDLINE=9731427; PubMed=9169421;
RA Pirozzi G., McConnell S.J., Uveges A.J., Carter J.M., Sparks A.B.,
RA Kay B.K., Fowlkes D.M.,
RT "Identification of novel human WW domain-containing proteins by
RT cloning of ligand targets."
RL J. Biol. Chem. 272:14611-14616(1997).
DR EMBL; U96115; AAC51326.1;
DR InterPro; IPR000619; Guanylate_kin.
DR InterPro; IPR002349; WW_domain.
DR Pfam; PF00397; WW; 1.
DR PRINTS; PR00403; WMDOMAIN.
DR SMART; SM00072; GUKC; 1.
DR SMART; SM00456; WW; 1.
DR PROSITE; PS00552; GUANYLATE_KINASE_2; 1.
DR PROSITE; PS01159; WW_DOMAIN_1; 1.
DR PROSITE; PS50020; WW_DOMAIN_2; 1.
DR NON_TER 1
FT NON_TER 1
FT NON_TER 224
SQ SEQUENCE 224 AA; 24816 MW; 42861373E3DFD626 CRC64;

Query Match 52.6% Score 50.5; DB 4; Length 224;
Best Local Similarity 61.1% Pred. No. 2.1;
Matches 11; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

Oy 1 DSEDEEHTITDTLPP 18
   1 1 1111 : 11 11
Db 103 DSGDEEHT-LOETLPP 119

RESULT 6
ID 043863 PRELIMINARY; PRT; 677 AA.
AC 043863;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MEMBRANE ASSOCIATED GUANYLATE KINASE 1 (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
RP MEDLINE=97369492; PubMed=9225980;
RA Margolis R.L., Abraham M.R., Gatchell S.B., Li S.H., Kidwai A.S.,
RA Breschel T.S., Stine O.C., Callahan C., McInnis M.G., Ross C.A.;

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RT "cGNAs with long CAG trinucleotide repeats from human brain.";
RL Hum. Genet. 100:114-122(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-9831405; PubMed-9647693;
RA Wood J.D., Yuan J., Margolis R.L., Colomer V., Duan K., Kushi J.,
RA Kamlinski Z., Kleiderlein J.J., Sharp A.H., Rose C.A.;
RT "Atrophin-1, the DRLA gene product, interacts with two families of WW
RT domain-containing proteins.";
DR MOl. Cell. Neurosci. 11:149-160(1998).
DR EMBL; U80754; AAC04844.1;
DR InterPro; IPR000619; Guanylate_kin.
DR InterPro; IPR001478; PDZ.
DR InterPro; IPR001202; WW.
DR InterPro; IPR002349; WW_domain.
DR Pfam; PF00595; PDZ; 2.
DR Pfam; PF00397; WW; 2.
DR PRINTS; PR00403; WMDOMAIN.
DR SMART; SM00072; GucK; 1.
DR SMART; SM00228; PDZ; 2.
DR SMART; SM00456; WW; 2.
DR PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
DR PROSITE; PS50106; PDZ; 2.
DR PROSITE; PS01159; WW_DOMAIN_1; 2.
DR PROSITE; PS50020; WW_DOMAIN_2; 2.
RW Kinase.
FT NON_TER
FT TER
SQ SEQUENCE 677 AA; 677 677 74507 MW; 9BAC9E8AC499D047 CRC64;

Query Match 52.6%; Score 50.5; DB 4; Length 677;
Best Local Similarity 61.1%; Pred. No. 6.8;
Matches 11; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

OY 1 DSEDEDEHTITDTFLP 18
||| |||| : : ||||
DB 105 DSGEQEHT-LOETALPP 121

RESULT 7
O960Z8 PRELIMINARY; PRT; 1160 AA.
AC O960Z8;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Mag1-1A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Laura R.P., Lasky L.A.;
RT "Mag1-1: a widely expressed, alternatively spliced tight junction
RT protein.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF401655; AAK94065.1;
DR EMBL; AF401655; AAK94065.1;
DR EMBL; AF401655; AAK94065.1;
SQ SEQUENCE 1160 AA; 126958 MW; 78FE5B621AC295B0 CRC64;

Query Match 52.6%; Score 50.5; DB 4; Length 1160;
Best Local Similarity 61.1%; Pred. No. 12;
Matches 11; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

OY 1 DSEDEDEHTITDTFLP 18
||| |||| : : ||||
DB 254 DSGEQEHT-LOETALPP 270

RESULT 8
075085

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ID Q75085 PRELIMINARY; PRT; 1256 AA.
 AC Q75085;
 DT 01-NOV-1998; TREMBLrel. 08, Created)
 DT 01-NOV-1998; TREMBLrel. 08, Last sequence update)
 DT 01-DEC-2001; TREMBLrel. 19, Last annotation update)
 DE BAIL-ASSOCIATED PROTEIN 1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RX MEDLINE=98321473; PubMed=9647739;
 RA Shiratsubo T., Futamura M., Oda K., Nishimori H., Nakamura Y.,
 RA Tokino T.
 RT Cloning and characterization of BAIL-associated protein 1: a PDZ domain-
 RT containing protein that interacts with BAIL.
 RL Biochem. Biophys. Res. Commun. 247:597-604(1998).
 DR EMBL; AB010894; BAA32002.1; -;
 DR HSP; P31016; 1BE9.
 DR InterPro; IPR000619; Guanylate_kin.
 DR InterPro; IPR001478; PDZ.
 DR InterPro; IPR001202; WW.
 DR InterPro; IPR002349; WW_domain.
 DR Pfam; PF00625; Guanylate_kin; 1.
 DR Pfam; PF00595; PDZ; 6.
 DR Pfam; PF00397; WW; 2.
 DR PRINTS; PR00403; WWDOMAIN.
 DR SMART; SM00072; GUKC; 1.
 DR SMART; SM00228; PDZ; 6.
 DR SMART; SM00456; WW; 2.
 DR PROSITE; PS00856; GUANYLATE_KINASE_1; 1.
 DR PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
 DR PROSITE; PS50106; PDZ; 6.
 DR PROSITE; PS01159; WW_DOMAIN_1; 2.
 DR PROSITE; PS50020; WW_DOMAIN_2; 2.
 SQ SEQUENCE 1256 AA; 136981 MW; 83FADE2091A4C8E4 CRC64;

Query Match 52.6%; Score 50.5; DB 4; Length 1256;
 Best Local Similarity 61.1%; Pred. No. 13;
 Matches 11; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

Qy 1 DSEDEEHTIITDTELP 18
 Db 254 DSGEQEHT-LQETALPP 270

RESULT 9
 Q96Q29 PRELIMINARY; PRT; 1287 AA.
 AC Q96Q29;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE MAGI-1B ALPHA BETA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Laura R.P., Lasky L.A.;
 RT "MAGI-1: a widely expressed, alternatively spliced tight junction
 RT protein."
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF401654; AAK94064.1; -;
 SQ SEQUENCE 1287 AA; 140439 MW; C676655657BDE0D5 CRC64;

Query Match 52.6%; Score 50.5; DB 4; Length 1287;
 Best Local Similarity 61.1%; Pred. No. 13;

Matches 11; Conservative 2; Mismatches 4; Indels 1; Gaps 1;
 Qy 1 DSEDEEHTIITDTELP 18
 Db 254 DSGEQEHT-LQETALPP 270

RESULT 10
 Q96Q27 PRELIMINARY; PRT; 1462 AA.
 AC Q96Q27;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE MAGI-1C BETA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Laura R.P., Lasky L.A.;
 RT "MAGI-1: a widely expressed, alternatively spliced tight junction
 RT protein."
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF401656; AAK94066.1; -;
 SQ SEQUENCE 1462 AA; 161609 MW; 2E98A448A9E7DF89 CRC64;

Query Match 52.6%; Score 50.5; DB 4; Length 1462;
 Best Local Similarity 61.1%; Pred. No. 15;
 Matches 11; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

Qy 1 DSEDEEHTIITDTELP 18
 Db 254 DSGEQEHT-LQETALPP 270

RESULT 11
 Q96AG1 PRELIMINARY; PRT; 526 AA.
 AC Q96AG1;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE HYPOTHETICAL 58.9 KDA PROTEIN (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=EYE, AND RETINOBLASTOMA;
 RA Strausberg R.;
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC017179; AAH17179.1; -;
 KW Hypothetical protein.
 FT NON_TER 1
 SQ SEQUENCE 526 AA; 58854 MW; 555A6529B6CEB211 CRC64;

Query Match 51.6%; Score 49.5; DB 4; Length 526;
 Best Local Similarity 55.6%; Pred. No. 7.6;
 Matches 10; Conservative 3; Mismatches 0; Indels 5; Gaps 1;

Qy 1 DSEDEEHTIITDTELP 18
 Db 210 DSDDEE-----DTEIPP 222

RESULT 12
 Q91LG7 PRELIMINARY; PRT; 1044 AA.
 ID Q91LG7

AC 091LG7;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DE 0973;
 OS White spot syndrome virus (WSSV).
 OC Viruses; Unassigned viruses.
 OX NCBI_TaxID=92652;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-21342372; PubMed-11448154;
 RA van Hulten M.C.W., Witteveldt J., Peters S., Kloosterboer N.,
 RA Tarchini R., Fiers M., Sandbrink H., Lankhorst R.K., Vlak J.M.,
 RT "The white spot syndrome virus DNA genome sequence.",
 RL Virology 286:7-22(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA van Hulten M.C.W., Witteveldt J., Peters S., Kloosterboer N.,
 RA Tarchini R., Fiers M., Sandbrink H., Lankhorst R.K., Vlak J.M.,
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL, AF369029; MAK7742.1;
 SO SEQUENCE 1044 AA; 117929 MW; 9E4E3EC52320B3E CRC64;

Query Match 51.0%; Score 49; DB 12; Length 1044;
 Best Local Similarity 66.7%; Pred. No. 19;
 Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 DSEDEEHITITDTE 15
 DB 152 DSEEEEDITVDDE 166

RESULT 13
 ID 097806 PRELIMINARY; PRT; 585 AA.
 AC 097806;
 DT 01-OCT-2001 (TREMBLrel. 18, Created)
 DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE FERREDOXIN OXIDOREDUCTASE.
 GN TVG1406112.
 OS Thermoplasma volcanium.
 OC Archaea; Euryarchaeota; Thermoplasmatales; Thermoplasmaceae;
 OX Thermoplasma
 NCBI_TaxID=50339;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-GSSI / DSM 4299 / JCM 9571;
 RA MEDLINE-20570466; PubMed-11121031;
 RA Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S.,
 RA Kawashima T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.,
 RA Nunoshima T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.,
 RT "Archaeal adaptation to higher temperatures revealed by genomic
 sequence of Thermoplasma volcanium.",
 RT Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).
 DR EMBL, AF000996; BAB60501.1;
 DR InterPro: IPR002869; POR.
 DR InterPro: IPR002860; POR_N.
 DR Pfam: PF01558; POR_1.
 DR Pfam: PF01555; POR_N; 1.
 KW Complete proteome.
 SO SEQUENCE 585 AA; 63978 MW; DD061F862266DFCD CRC64;

Query Match 50.0%; Score 48; DB 17; Length 585;
 Best Local Similarity 50.0%; Pred. No. 15;
 Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

OY 1 DSEDEEHITITDTELP 18
 DB 395 DNEEDYKRYITDTGISP 412

RESULT 14
 ID 099K58 PRELIMINARY; PRT; 1174 AA.
 AC 099K58;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE SIMILAR TO FIBULIN 2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-MAMMARY TUMOR. WAP-TGF ALPHA MODEL. 7 MONTHS OLD. GROSS
 RC TISSUE-;
 RA Strausberg R.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL, BC005443; ANH05443.1;
 DR HSPF, P00736; IAPQ.
 DR InterPro: IPR000020; Anaphylatoxin.
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR001881; EGF_Ca.
 DR Pfam, PF00808; ANATO. 2.
 DR Pfam, PF00808; EGF. 6.
 DR SMART, SM00104; ANATO; 3.
 DR SMART, SM00181; EGF. 11.
 DR SMART, SM00179; EGF_CA; 9.
 DR PROSITE, PS01177; ANAPHYLATOXIN_1; 3.
 DR PROSITE, PS01178; ANAPHYLATOXIN_2; 3.
 DR PROSITE, PS00010; ASX_HYDROXYL; 5.
 DR PROSITE, PS01186; EGF_2; 5.
 DR PROSITE, PS01187; EGF_CA; 9.
 DR Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat.
 SO SEQUENCE 1174 AA; 126460 MW; 8D628AC710FBA6B8 CRC64;

Query Match 49.5%; Score 47.5; DB 11; Length 1174;
 Best Local Similarity 50.0%; Pred. No. 38;
 Matches 9; Conservative 4; Mismatches 2; Indels 3; Gaps 1;

OY 1 DSEDEEHITITDTELP 18
 DB 274 DEEEEBETIVTE---PP 288

RESULT 15
 ID 006810 PRELIMINARY; PRT; 360 AA.
 AC 006810;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CHROMOSOME XVI COSMID 9513.
 GN OPI2 OR P9513.9 OR YPR075C.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-S288C (AB972);
 RA Couch J.;
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-S288C (AB972);
 RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,
 RA Favellio A., Fulton L., Gattung S., Greco T., Kirsten J., Kucaba T.,
 RA Hallsworth K., Hawkins J., Hillier L., Jier M., Johnson D.,
 RA Johnston L., Langston Y., Latreille P., Le T., Mardis E., Menezes S.,

RA Miller N., Nhan M., Pauley A., Peluso D., Rifkin L., Riles L.,
RA Taich A., Trevisani E., Vignati D., Wilcox L., Wohlman P., Vaudin M.,
RA Wilson R., ~~Mc~~Gerston R.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
[3]
RL SEQUENCE FROM N.A.
RP STRAIN-S288C (AB972);
RC Waterston R.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
[4]
RP SEQUENCE FROM N.A.
RA Edwards M.C., Lisegeois N., Horecka J., Depinho R.A., Sprague G.F.,
RA Tyers M., Ellledge S.J.;
RL Genetics 0-10-0(1997);
DR EMBL: U50683; AAB08126.1; --
DR EMBL: AF016263; AAB81506.1; --
RL SGD: S0006279; OPY2.
SQ SEQUENCE 360 AA; 38901 MW; 6D44AFA25042FFB CRC64;

Query Match	49.0%	Score 47	DB 3	Length 360
Best Local Similarity	47.1%	Pred. No. 13		
Matches	8	Conservative	4	Mismatches
			5	Indels
			0	Gaps
			0	

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QY      1 DSEDEEHTIITDTLP 17
        | : ||| : | | : |
DB     318 DEDDDEEGSFILDLIP 334
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Search completed: September 20, 2002, 10:31:03
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